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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 28, 2004, 17:51:02 ; Search time 3.97883 Seconds (without alignments) 2975.262 Million cell updates/sec Run on:

194 1'GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33 US-10-019-823B-2 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s: geneseqp1990s: geneseqp2000s: geneseqp2001s: geneseqp2001s: geneseqp2003bs: geneseqp2003bs: A Geneseq 23Sep04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aab66900 Insectici	N	Aae36261 Insectici	Aae36295 Insectici	Aae36260 Insectici		Aae36259 Insectici	529	Aae36292 Insectici	Aae36287 Insectici	Aae36289 Insectici	Aae36263 Insectici	28	Aae36288 Insectici	Aae36296 Insectici	Aae36286 Insectici	5291 I	Aae36264 Insectici	Aae36285 Insectici	Aae36262 Insectici	Aae36297 Insectici	Aae36298 Insectici	Aae36293 Insectici	Aab66901 Insectici	Aae36281 Insectici
QI	6699	AAE36283	AAE36261	AAE36295	AAE36260	529	525	AAE36290	AAE36292	AAE36287	AAE36289	AAE36263	AAE36284	22	529	528	AAE36291	AAE36264	AAE36285	AAE36262	AAE36297	AAE36298	AAE36293	AAB66901	AAE36281
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Length	33	33	34	34	34	34		34		34	34	34	34	34	34	34	34	34	34	34	34	34	34	35	35
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Aae36265 Insectici Aae36282 Insectici AAb66899 Insectici Abb88548 Janus fac	318 318 318	54 Conus 50 Janus 37 Atraco 35 Ravent	0.000	Abb88713 Conus ema Adp31056 Human sec Abb88898 Conus vir Abg99796 Conus sp
AAB36265 AAB36282 AAB6899	ABB8854 AAR3931 AAR3931 ABG9978	ABG99 ABB88 ADL11 ADL11	ABG9978 ABG9945 ABB8888 ABB8892	ABB88713 ADP31056 ABB88898 ABG99796
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RESULT AAB669	RESULT 1 AAB66900	
e X	AAB66900 standard; peptide; 33 AA.	
AC	AAB66900;	
×		
ΤΩ	12-APR-2001 (first entry)	
×		
DE	Insecticidal protein #2.	
XX		
K	Insecticide, transgenic plant; insect-resistance.	tance.
×		
SO	Paecilomyces sp.	
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Md	WO200100841-A1.	
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PD	04-JAN-2001.	
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PF	23-JUN-2000; 2000WO-GB002457.	
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PR	29-JUN-1999; 99GB-00015215.	
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PA	(ZENE ) ZENECA LTD.	
×		
Ы	J,	, EA, W
ΡΙ	Vincent JL, Lee MD;	
X		
R	WPI; 2001-123015/13.	

Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production. 

Warner SAJ;

Claim 3; Page 30; 72pp; English.

The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

Sequence 33 AA;

ö 0; Gaps Query Match
100.0%; Score 194; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.6e-15;
Matches 33; Conservative 0; Mismatches 0; Indels

GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33

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100.0%; Pred. No. 9.6e-15;
live 0; Mismatches 0;
GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
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Matches
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
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                                                                                                                                                                               New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
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                                        30-MAY-2002; 2002WO-GB002666.
                                                                  07-JUN-2001; 2001GB-00013900.
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                                                                                             (SYGN ) SYNGENTA LTD
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                                                                                                                                                      WPI; 2003-175137/17.
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Best Local Similarity
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insectlicidal activity. The present sequence is
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100.0%; Pred. No. 9.9e-15;
ive 0; Mismatches 0;
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 AAE36294 standard; peptide; 34 AA.
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                                                                                                                                                                                                                                                                        2002WO-GB002666.
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                                                                                                                                                                                                                                                                                                                                                                              Viner R;
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                                    AAE36294;
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invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
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terminus, useful as an active ingredient of a pesticide.
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Best Local Similarity 100.
Matches 33; Conservative
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Best Local Similarity 100.
Matches 33; Conservative
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                                                                                          insecticidal protein
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                                                                                                                             Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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RESULT 6 AAE36294

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
    Antibodies raised to the insecticidal proteins can be used to idenother proteins with insecticidal activity. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 34;
                                                                                                                                                              Indels
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                                                                                                                       Length
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terminus, useful as an active ingredient of a pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 194; DB 6;
100.0%; Pred. No. 9.9e-15;
. . Mismatches 0;
                                                                                                                       Score 194; DB 6;
Pred. No. 9.9e-15;
                                                                                                                                                                                                                                     34
                                                                                                                                                                                             1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
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                                                                                                                                                                                                                        GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                     AAE36292 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 65; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE36287 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; pesticide.
                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2001; 2001GB-00013900.
                                                                                                                                                          33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insecticidal protein #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
                                         insecticidal protein
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                                                                                                               Query Match
Best Local Similarity
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                                                                                Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insecticidal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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                                                                                                                                                                                                                                                                                                       motif at the amino-terminus. Polymuclectide or DNA constructs of the invention are useful for producing plants or plant parts that are resistent to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
                                                                                                                                                                                                                                                                                      invention relates to insecticidal protein comprising an X-glycine
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                                                                                                                                                                                       New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 194; DB 6;
100.0%; Pred. No. 9.9e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                   Claim 1; Page 23; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insecticidal protein; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE36290 standard; peptide; 34
30-MAY-2002; 2002WO-GB002666
                                   07-JUN-2001; 2001GB-00013900
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Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insecticidal protein #20.
                                                                                                               Vincent JL, Viner R;
                                                                        (SYGN ) SYNGENTA LID
                                                                                                                                                                                                                                                                                                                                                                                                                              insecticidal protein
                                                                                                                                                      WPI; 2003-175137/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34 AA;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
                                                                                                                                        The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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terminus, useful as an active ingredient of a pesticide.
                                            New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
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100.0%; Pred. No. 9.9e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 194;
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                                                                                                         Example 1; Page 64; 67pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insecticidal protein; pesticide.
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                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
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                                                                                                                                                                                                                                                                                    insecticidal protein
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                WPI; 2003-175137/17.
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                         Sequence 34 AA;
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AAE36263
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terminus, useful as an active ingredient of a pesticide.
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100.0%; Pred. No. 9.9e-15;
ive 0; Mismatches 0;
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                                                                                               Insecticidal protein; pesticide.
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Best Local Similarity 100.
- Local 33; Conservative
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                                                        Insecticidal protein #17
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                                                                                                                                    Unidentified
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RESULT 11 AAE36289

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
                                                                                                                                                                                                                                                         New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
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100.0%; Pred. No. 9.9e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                        Example 1; Page 64; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE36296 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insecticidal protein, pesticide.
                                                                                                30-MAY-2002; 2002WO-GB002666.
                                                                                                                                07-JUN-2001; 2001GB-00013900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2002; 2002WO-GB002666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-2001; 2001GB-00013900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insecticidal protein #26.
                                                                                                                                                                                          Vincent JL, Viner R;
                                                                                                                                                              (SYGN ) SYNGENTA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    insecticidal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vincent JL, Viner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYGN ) SYNGENTA LID
                                                                                                                                                                                                                          WPI; 2003-175137/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-175137/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34 AA;
                                 WO200298911-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200298911-A2
     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified,
                                                                12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE36296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 Similarity 100.0%; Pred. No. 9.9e-15; 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 194; DB 6;
100.0%; Pred. No. 9.9e-15;
iive 0; Mismatches 0;
                                               1 GKICTPAGVKCPALPCCPGLRCIGGVNNKVCR 33
                                                                           GKICTPAGVKCPALFCCPGLRCIGGVNNKVCR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
                                                                                                                                                         AAE36284 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 62; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE36288 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                     Insecticidal protein; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insecticidal protein; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2002; 2002WO-GB002666
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-2001, 2001GB-00013900.
                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein #18.
                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vincent JL, Viner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticidal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-175137/17
                                                                                                                                                                                                                                                                                                                                                  WO20029891-1-A2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34 AA;
                                                                                                                                                                                                                                                     Insecticidal
                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                       26~JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insecticidal
                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2003
                                                                                                                                                                                         AAE36284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE36288
Best Local
Matches
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Example 1; Page 66; 67pp; English

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Gaps

g

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
*8888888888
```

Sequence 34 AA;

Gaps . . Length 34; Query Match
100.0%; Score 194; DB 6; Length 34
Best Local Similarity 100.0%; Pred. No. 9.9e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 1 GKICTPAGVKCPAALPCCPCIRCIGGVNNKVCR 33 à

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Search completed: October 28, 2004, 18:19:40 Job time : 4.97883 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 28, 2004, 18:05:43; Search time 0.88081 Seconds (without alignments) 3604.811 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-019-823B-2 194 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

SERV

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	in Ia -	probable membrane	Fibropellin C prec	mu-conotoxin GS -	aptotoxin III - tr	hypothetical prote	_	tein (	protein C05B5.5 [i	recept	sperm mitochondria	tin-like	Notch homolog prot	notch protein homo	notch-1 protein -	hypothetical prote	osmotin protein ho		4 OE	Z	epidermal growth f	acroglob	platelet aggregati	ecific p	hypothetical prote	protein Y47D3B.6 [	1 3 prot	notch3 protein - h	CEF-10 protein pre
SUMMARIES	QI	A40136	S48564	A48836	A31043	E44007	T08724	T23472	843572	E88571	T30346	T10081	T04166	T30201	S18188	A46019	H75335	T03287	T22025	D89711	A87722	EGHU	A53102	H43019	825773	T26957	E88597	4530	854	4142
	DB	7	7	7	N	7	7	~	N	N	N	N	~	N	N	~	N	C)	N	~1	7	Н	H	7	~	N	N	N	~	N
	Query Match Length	12	422	-	34	37	417	1221	m	m	m	$\mathbf{r}$	m	35	m	53	m	$\overline{}$	$\circ$	0	S	20	₹*	73	74	9	283	н	32	7
de	Query	m	O	O	0	σ	29.6	σ	σ	σ	σ	α	α	α	ω	œ	æ	æ	œ	œ	œ	œ	æ	7	$\sim$	~	^	$\sim$	7	~
	Score		60		58.5	59	57.5	57	٠.	56.5	9	56	. 29	26	26	26	52	4.	4.	4.	54.5	4.	4,	54	54	54	54	54	54	23
	Result No.		04	ო	4	Ŋ	9	7	α	σv	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

protein C (activat	Delta-4 protein -	crumbs protein - f	Xotch protein - Af	hypothetical prote	alpha-2-macroglobu	alpha-2-macroglobu	metallothionein A	platelet aggregati	conserved hypothet	Motch B protein -	E2 glycoprotein pr	transmembrane prot	pathogenesis-relat	osmotin-like prote	osmotin-like prote
õ	C7569	A35672	435844	T26950	802392	825111	A25775	343019	AD0652	A49175	847423	842612	831829	528001	330144
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1 KXE	2 JC7	2 A35	2 A3	2 T	1 8	Η	7	6	2 A	7 7	2	Š C	2	2	7
-	23	(7)	2524 2 A3	596 2 T	4544 1 S	4545 1 8	64 2 1	71 2 G	134 2 AI	1203 2 A	α	2437 2 5	(1)	238 2 S	246 2 8
-	686 2 J	2139 2	7	596 2	4544 1	4545 1	64 2	71 2	134 2	N	1449 2	2437 2	233 2	238 2 8	246 2
-	686 2 J	2139 2	2524 2 7	27.1 596 2	27.1 4544 1	4545 1	64 2	71 2	134 2	1203 2	1449 2	2437 2	26.5 233 2	238 2 8	26.5 246 2 3

# ALIGNMENTS

RESULT 1 A40136 fibropallin Ia - sea urchin (Strongylocentrotus purpuratus) NiAlternate names: epidermal growth factor homolog precursor NiAlternate names: epidermal growth factor homolog precursor NiAlternate names: strongylocentrotus purpuratus (purple urchin) C;Species: Strongylocentrotus purpuratus (purple urchin) C;Accession: A40136; B40136; C40136; A29316; A43131 C;Accession: A40136; B40136; C40136; A29316; A43131 R;Delgadillo-Reynoso, M.c.; Rollo, D.R.; Hursh, D.A.; Raff, R.A. C;Mol. Bvol. 29, 314-327, 1980 A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpus A;Accession: A40136 A;Accession: A40136 A;Status: preliminary
A, Molecule type: mRNA A, Residues: 1-14 < CDEL> A, Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061 A, Accession: B40136 A, Status: preliminary; not compared with conceptual translation A, Molecule type: DNA A, Residues: 181-251,329-370, 'R',372-408,'RA',411-441 < DE2> A, Accession: C40136 A, Status: preliminary; not compared with conceptual translation A, Molecule type: DNA
Ajkriducus N. / J. Andrews, M.E.; Raff, R.A. Science 237, 1487-1490, 1987 Bard encodes a polypeptide homologous to epidermal growth factor. AjRefession: A29316; MUID:87319677; PMID:3498216 AjRecession: A29316 AjRecession: A29316 AjRecession: Applicate type: mRNA AjResidues: Vpge: mRNA AjResidues: S', 280-481,786-1064 KHUR> AjResidues: S', 280-481,786-1064 KHUR> RjWunt, L.T.; Barker, W.C. Spillut, L.T.; Barker, W.C. Spillut, L.T.; Barker, W.C. Spillut, L.T. Agrange M.C. Spillut, L.T. Spillut, M.C. Spillut, L.T. Spillut, M.C. Spillut, L.T. Spillut, M.C. Spillut, M
A:71tle: Avidin-1ike domain in an epidermal growth factor homolog from a sea urchin. A:71tle: Avidin-1ike domain in an epidermal growth factor homolog from a sea urchin. A:71tle: annotation the sea urchin. A:71tle: annotation the season of

7

<EG19><EG20><EG21>

homology homology homology

homology

F;936-1064/Region:

F;902-933/Domain:

/Domain:

F;864-895,

Conservative

15;

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Local Similarity

Query Match Matches

<EG16> <EG14>

<EG15>

homology homology homology homology homology

F;598-629/Domain: B;636-667/Domain: B;634-705/Domain: B;712-743/Domain: B;750-781/Domain: E

F;788-819/Domain: F;826-857/Domain:

homology

F;484-515/Domain: F;522-553/Domain:

:522-553/Domain: :560-591/Domain:

<EG17> <EG18>

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aptotoxin III - trap-door spider (Aptostichus schlingeri)
NyAlternate names: insecticidal peptide Aps III
C;Species: Aptostichus schlingeri
C;Species: Aptostichus schlingeri
C;Accession: E44007
R;Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.
Toxicon 30, 1043-1050, 1992
A;Title: Identification of insecticidal peptides from venom of the trap-door spider, Apto A;Reference number: A44007, MUID:93069259; PMID:1440641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Conus geographus (geographus)
C.Species: Conus geographus (geography cone)
C.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C.Accession: A3104 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C.Accession: A3104 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C.Accession: A31043 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C.Accession: A31043 #sequence with the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:23-34,28-43,45-64,62-88,188-191,185-200,202-211,218-229,223-238,240-249,256-267,261-276
fide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor; ver
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A,Residues: 1-34 <YAN>
A,Cross-references: UNIPROT: P15472
A,Cross-references: UNIPROT: P15472
C,Superfamily: unassigned conotoxins
C,Superfamily: unassigned conotoxins
C,Reywords: carboxyglutamic acid; hydroxyproline; myotoxin; sodium channel F;0.11/Modified site: 4-hydroxyproline (Pro) #status experimental F;32/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental F;34/Modified site: amidated carboxyl end (Val) #status absent
A;Cross-references: UNIPROT:P49013; GB:L07045; NID:g310659; PID:g310660
A;Note: sequence extracted from NCBI backbone (NCBIN:132724, NCBIP:132725)
F;1-18/Domain: signal sequence #status predicted <5IG>F;1-18/Domain: signal sequence #status predicted <5IG>F;19-570/Product: fibropellin C #status predicted <FIB>F;19-570/Product: fibropellin C #status predicted <FIB>F;19-54/Domain: EGF homology <EGI>F;19-54/Domain: EGF homology <EGI>F;14-249/Domain: EGF homology <EGI>F;21-249/Domain: EGF homology <EGI>F;22-287/Domain: EGF homology <EGI>F;280-325/Domain: EGF homology <EGGS>F;266-401/Domain: EGF homology <EGI>F;466-401/Domain: EGF homology <EGI>F;460-401/Domain: EGF homology <EGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Residues: 1-37 <SKI>
A;Cross-references: UNIPROT:P49268; PIDN:AAB24051.1; PID:g259281
A;Note: sequence extracted from NCBI backbone (NCBIP:119526)
C;Keywords: disulfide bond; toxin; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 570;
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Pred. No. 12;
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Pred. No. 1.
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1 Similarity 44.8%;
13; Conservative
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Best Local Similarity
Matches 13; Conserv
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Matches
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448836
fibropellin C precursor - sea urchin (Strongylocentrotus purpuratus)
NiAlternate names: EGF repeat-containing protein; epidermal growth factor-related protein
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Accession: A48836
R;Bisgrove, B.W.; Raff, R.A.
Dev. B.O.: 526-538, 1993
A;Title: The SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing
A;Reference number: A48836
A;Accession: A48836
A;Accession: A48836
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-570 cBIS>
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A;Molecule type: DNA
A;Residues: 1-422 <PAU>
A;Cross-references: UNIPROT:Q05790; EMBL:U14913; NID:g544497; PID:g544518; GSPDB:GN00012
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
57,411-466,468-477,498-495/Disulfide bonds: #status predicted
F;48-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Disul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YLR213c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L8167.22
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: 848564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 ICAPGFDGLNCENNIDECASRPCONGAVCVDGVNGFVC 466
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Pred. No. 9.3;
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39.5%; Pred. No. e...
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A)Cross-references: SGD:S0004203 A;Map position: 12R C;Keywords: transmembrane protein

A, Gene: SGD: CRR1; MIPS: YLR213c

30.9%; 40.6%;

CTPAGVKCPAALPCC----

13; Conservative

Best Local Similarity

Matches

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Query Match

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Rjanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A;75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.vustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A, Accession: T30346
A, Accession: T30346
A, Recture: pre-liminary, translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residuces: 1-130 < GRAA
A, Cross-references: UNIRKOT:093105; EMBL:U72939; NID:91620749; PID:91620750; PIDN:AAB1709
C, Superfamily: insulin receptor; protein kinase homology
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E88571
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C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 22-Oct.1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                              DB 2;
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29.1%; Score 56.5; D
Best Local Similarity 30.4%; Pred. No. 31;
Matches 14; Conservative 2; Mismatches
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    A Accession: $43572
A Status: preliminary
A Modecule type: DNA
A Residues: 1-585 < MOR>
A Cross-references: EMBL: 232679
C Genetics:
A :Introns: 35/2; 218/3; 292/2; 328/1; 442/2
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nes 15; Conservative
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Matches 14; Conservative
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Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipacession: T23472
Submitted to the EMBL Data Library, July 1996
A;Reference number: Z19745
A;Reference number: Z19745
A;Reference number: Z19745
A;Reference number: DAA
A;Referen
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A,Map position: 4
A,Introns: 26/1; 103/1; 170/1; 640/1; 802/2; 831/1; 864/3; 891/3; 908/1; 938/2; 980/1;
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Cispecies: Homo sapiens
Cispecies: Homo sapiens
Cispecies: Homo sapiens
Cispecies: Lispecies: Lispeci
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sacession: S43572
R;Mortimore, B
submitted to the EMBL Data Library, April 1994
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Pred. No. 49;
3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 KLCCPAGIFGPSCLPCPGGIERPCGGYGQCEGEGIRGGSGHCDCQ 184
Score 58; DB 2; Length 37;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57.5; DB 2; Length 4 Pred. No. 18; 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CPGLRCIGGVNNKVCR 33
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
T23472
hypothetical protein K08E7.5 - Caenorhabditis elegans
                                                                                                                                                                          4 CTPAGVKCPAALPCCPG-----LRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                  1 CNSKGTPCTNADECCGGKCAYNVWNCIGGGCSKTC 35
                                              Pred. No. 2.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             971 CAPPAPCCLPTIPCCPPIPCC--PQPKIC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein DKFZp566D213.1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: clone K08E7
    29.9%;
llarity 37.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31.1%;
Matches 14; Conservative
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Best Local Similarity 34.5%;
Matches 10; Conservative
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    Query Match
Best Local Similarity
Matches 13; Conserv
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28.9%;
ilarity 36.8%;
Conservative 2
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Best Local Similarity 36.8 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             notch protein homolog - rat
A; Reference number: Z20775
                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 14; Conserv
                                                                                                                                                                                                                                                                                 Query Match
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T30201
Notch homolog protein - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Species: Halocynthia roretzi
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2002
C;Accession: T30201
R;Hori, S:, Saitoh, T; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaumatin-like protein - rice
Cispecies: Oryza sativa (rice)
Cjate: Jahr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CjAccession: T04166
R;Cole, K.C.; Velazhahan, R.; Anuratha, C.S.; Muthukrishnan, S.
submitted to the EMBL Data Library, November 1996
A;Description: Induction of thaumatin-like proteins (TLPs) in Rhizoctonia solani- infect
A;Reference number: Z15250
                                                                                                                              C;Accession: T10081; A37199
R;Kleene, X.C.; Smith, J.; Bozorgzadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel Bob. Biol. 137, 395-402, 1990
A;Title: Sequence and developmental expression of the mRNA encoding the seleno-protein d A;Reference number: A37199; MUD:90152148; PMID:2303168
A;Accession: T10081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .Cross-references: UNIPROT:004364; EMBL:U77657; NID:92062388; PIDN:AAB53368.1; PID:9206
                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
?Residues: 1-6,'X', 8-16,'X', 18-33,'X',35-197 <KLE1>
;Cross-references: UNIPROT:P15265; EMBL:M29603; NID:g199088; PIDN:AAA53045.1; PID:g5672
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain CD-1
A;Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAA53045.1, the selenocysteine UGA
A;Accession: A37199
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                                                                                       sperm mitochondrial capsule selenoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A,Residues: 55-197 <KLE2>
A,Cross-references: GB:M29603; NID:g199088
A,Note: the authors translated the codon TGT for residue 112 as
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 2; Length 197;
Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: MCS
A;Genome: nuclear
C;Keywords: mitochondrion; selenocysteine; sperm
F;7,17,34/Modified site: selenocysteine #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 «COL»
A;Cross-references: UNIPROT:004364; EMBL:U77657; NII
C;Superfamily: thaumatin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCPKGGPRCATAITPOCPSELRAPGGCNN 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCPKSPCCPPKSPCCPPKPC 106
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Best Local Similarity 45.0%;
Matches 9; Conservative C
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Matches 14, Conserv
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NiAlternate names: motth protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 16-Aug-2004
C;Accession: A46019; S25144; Cq9175; B46438; A46438; PHI559; S32109
R;del Ano, F. F.; Gendron-Maguire, M.; Swiatek, P.U.; Jenkins, N.A.; Copeland, N.G.; GridJ
Genomics 15, 259-264, 1993
A;Ittle: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I
A;Reference number: A46019; MuID:93194170; PMID:8449489
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;
A,Accession: T30201
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-2352 «HOR>
A,Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1
C,Genetics:
A,Gene: Notch
C,Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Rattus norvegicus (Norway rat)
C.Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C.Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C.Accession: 518188
R.Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A.Pitler. A homolog of Drosophila Notch expressed during mammalian development.
A.Reference number: 518188; WUID:92111383; PMID:1764995
A.Accession: 518188.
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homology; EGF homology
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                                                                                                                                                                                                                                               Length 2352;
                                                                                                                                                                                                                                                                                                       14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  593 CTPGYTGEHCDTDINECDSNPCMNGATCQNEVNNFVCQ 630
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                                                                                                                                                                                                                                                                                                                                                             4 CTP--AGVKCPAAL----PCCPGLRCIGGVNNKVCR 33
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                                                                                                                                                                                                                                            Score 56; DB 2; I
Pred. No. 1.1e+02;
2; Mismatches 14;
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y 36.8%; Pred. No. 1...
2; Mismatches
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homology <AN5>
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A,Residues: 1-2531 WREI>
A,Residues: 1-2531 WREI>
C,Crose references: EMBL:X57405; NID:957634;
C,Superfamily: notch protein; ankyrin repeat
F;987-1018/Domain: EGF homology xEGF1>
F;1025-1056/Domain: EGF homology xEGF2>
F;1233-1264/Domain: EGF homology xEGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F.1917-1949/Domain: ankyrin repeat homology F.1950-1982/Domain: ankyrin repeat homology F.1950-1984-2016/Domain: ankyrin repeat homology F.2017-2049/Domain: ankyrin repeat homology F.2050-2082/Domain: ankyrin repeat homology
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A; Molecule Lype: mRNA
A; Residues: 1161-1547 c.LAR>
A; Residues: 1161-1547 c.LAR>
A; Estimates: 1161-1547 c.LAR>
A; Estimated: embryo
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP:126159)
B; Kopan, R; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A; Title: Mouse notch: expression in hair follicles correlates with cell fate determinating A; Reference number: A46438; MUID:93252998; PMID:8486742
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Molecule type: nucleic acid
A)Rolecules: 1865-1932, RR', 1935-1937, L', 1938-1967, L', 1969-2044, IE', 2047-2052, 'S', 2054
A)Residues: 1865-1932, 'RR', 1935-1937, L', 1938-1967, L', 1969-2044, 'IE', 2047-2052, 'S', 2054
A)Experimental source: embryo
A)Roles: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C;Comment: This protein has many EGF repeate and lin-12[#1172]/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe
A; Molecule type: mRNA
A; Residues: 1551-2108, 'O', 2110-2114,'ALP',2118-2170 <FRA>
A; Cross-references: BMBL:211886
B; Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A; Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A; Reference number: A49178; MUID:93178563; PMID:8440332
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in; ankyrin repeat homology; EGF homology
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A,Status: preliminary; nucleic acid sequence not shown
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F;1149-1180/Domain: EGF homology <EG17>
F;1187-1218/Domain: EGF homology <EG18>
F;1187-1218/Domain: EGF homology <EG18>
F;1253-1383/Domain: EGF homology <EG18>
F;1351-1425/Domain: EGF homology <EGF>
F;1391-1425/Domain: EGF homology <EGF>
F;1917-1948/Domain: ankyrin repeat homology <AMI>F;1943-1981/Domain: ankyrin repeat homology <AMI>F;2016-2048/Domain: ankyrin repeat homology <AMI>F;2016-2048/Domain: ankyrin repeat homology <AMI>F;2016-2048/Domain: ankyrin repeat homology <AMI>F;2049-2081/Domain: ankyrin repeat homology <AMI>F;2049-2048/Domain: ankyrin repeat homology <AMI>F;2049-2048/Domain: ankyrin repeat homology <AMI>F;2049-2048/Domain: ankyrin repeat homology <AMI>F;2049-2048/Domain: ankyrin repeat homology <AMI>F;20
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95-826/Domain: EGF homology <EG10>
95-904/Domain: EGF homology <EG11>
11-942/Domain: EGF homology <EG12>
49-980/Domain: EGF homology <EG13>
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F;1063-1094/Domain: EGF
F;1149-1180/Domain: EGF
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A;Gene: notch-1
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245 CLPGFAGONCEENVDDCPGNNCKNGGACVDGVNTYNCR 282

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Search completed: October 28, 2004, 18:31:45 Job time : 2.88081 secs

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October 28, 2004, 18:10:58 ; Search time 3.0145 Seconds (without alignments) 3549.224 Million cell updates/sec
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1: /cgr2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
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14: /cgn2_6/prodata/2/pubpaa/USIOD_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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194
1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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	Description	Sequence 3, Appli		1 Seguence 57		ഗ		B-137 Sequence 137, App	S)	Sequence 497,	Sequence 247,		Sequence 37,	Sequence 37,
SUPERFIEE	ID	US-09-894-882-3	US-09-894-882-4	US-10-072-602B-57	US-10-072-602B-140	US-09-894-882-5	US-10-072-602	US-10-072-602B-137	US-09-894-882-	US-09-894-882-497	US-09-894-882-	US-10-123-155	US-10-146-731-37	US-10-140-472-37
	DB		o	14	14	σv	14	14	σ	σ	σ	14	14	14
	å Query Match Length DB	36	36	35	82	37	30	77	31	3	67	3501	3501	3501
d	Query Match	42.3	40.7	37.6	37.6	37.4	35.8	35.8	35.6	35.6	35.6	35.1	35.1	35.1
	Score	82	79	73	73	72.5	69.5	69.5	69	69	69	68	68	68
	Result No.	 		e	4	S	9	7	80	o,	10	11	12	13

Sequence 37, Appl Sequence 470, App Sequence 498, Appl Sequence 498, Appl Sequence 576, Appl Sequence 139, Appl Appl Sequence 139, Appl Appl Appl Sequence 139, Appl Appl Appl Appl Appl Appl Appl App	equence 133
US-10-141-761-37 US-10-142-865-37 US-10-137-871-37 US-10-140-923-37 US-10-141-756-37 US-10-141-756-37 US-10-141-756-37 US-10-141-756-37 US-10-141-756-37 US-10-142-865-37 US-10-142-865-37 US-09-894-882-496 US-09-894-882-498 US-09-894-882-498 US-09-894-882-498 US-09-894-882-498 US-09-894-892-274 US-10-128-555 US-10-184-644-493 US-10-184-644-493 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-5 US-09-900-449A-7 US-09-900-449A-7 US-10-123-155-139 US-10-140-472-139	-10-137-871-13
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ALIGNMENTS

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Sequence 3, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Genetix, Inc.
APPLICANT: Walker, Inc.
APPLICANT: Genetix, Inc.
APPLICANT: Gherex, Baide C.
APPLICANT: Gherex, Baidenero M.
APPLICANT: Gherex, Baidenero M.
APPLICANT: Gheres, Baidenero M.
APPLICANT: Gheres, Robert M.
APPLICANT: Shar, Greg S.
TITLE OF INVENTION: L'superfamily Conctoxins
TITLE OF INVENTION: 1. Superfamily Conctoxins
TITLE OF INVENTION: 1. Superfamily Conctoxins
FILE REFERENCE: 2314-238
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-16-29
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-36
PRIOR FILING DATE: 2001-0-39
PRIOR FILING DATE: 2001-0-39
PRIOR FILING DATE: 2001-10-39
PRIOR FILING DATE: 2001-10-39
PRIOR PRING DATE: 2001-10-39
PRIOR FILING DATE: 2001-10-39
PRIOR PRING DATE: 2001-10-39
PRIOR FILING DATE: 2001-01-39
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JS-09-894-882-3
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| Sequence 140, Application US/10072602B |
| Publication No. US20030109670A1 |
| GENERAL INFORMATION: |
| APPLICANT: University of Utah Research Foundation |
| APPLICANT: Olyera, Baldomero M. |
| APPLICANT: McIntosh, J, Michael |
| APPLICANT: Markins, Maren |
| APPLICANT: Markins, Maren |
| APPLICANT: Garrett, James E. |
| APPLICANT: Garrett, James E. |
| APPLICANT: Garrett, Grailey, Michaelle |
| APPLICANT: Schoenfeld, Robert M. |
| APPLICANT: Warker, Craig |
| APPLICANT: Schoenfeld, Robert M. |
| APPLICANT: Schoenfeld, Robert M. |
| APPLICANT: Warker, Craig |
| APPLICANT: Warker, Craig |
| APPLICANT: Warker, Caig |
| WARKEN TAING DATE: 2002-02-11 |
| WARKEN TAING DATE: 2002-02-11 |
| WARKEN TAING DATE: 2001-02-09 |
| WARKEN TAING DATE: 2001-02-03 |
| WARKEN TAING DATE: 2001-02-03 |
| WARKEN TAING DATE: 2001-
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Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
FRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 571
LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
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US-10-072-602B-140
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus lividus
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LENGTH: 82
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US-09-894-882-5
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ORGANISM: (
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                                                    Query Match 42.3%; Score 82; DB 9; Length 36; Best Local Similarity 51.5%; Pred. No. 0.022; Matches 17; Conservative 1; Mismatches 13; Indels
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APPLICANT: University of Utah Research Foundation
APPLICANT: Offerat, Inc.,
APPLICANT: Olivera, Baldomero M.
APPLICANT: Montrosh, J, Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Grilley, Michael
APPLICANT: Grilley, Michael
APPLICANT: Grilley, Michael
APPLICANT: Grilley, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Once, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conctoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/249
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLICATION NUMBER: US 60/245,714
PRIOR PLICATION NUMBER: US 60/247,714
PRIOR PLICATION NUMBER: US 60/247,714
PRIOR PRILING DATE: 2000-11-09
PRIOR PRILING DATE: 2000-11-09
PRIOR PRILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                         3 ICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
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US-10-072-602B-571
; Sequence 571, Application US/10072602B
; Publication No. US20030109670A1
                                                                                                                                                                                                                                                                                                                                                                                       US-09-894-882-4; Sequence 4, Application US/09894882; Patent No. US20021102607A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shetty, Reshma
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walker, Craig
Shetty, Reshma
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Best Local Similarity
Matches 17; Conserv
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LENGIH: 36
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APPLICANT:
APPLICANT:
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2 CGHSGAGC-YTRPCCPGLHCSGGQAGGLC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.5; DB 9; Length 37;
Pred. No. 0.27;
0; Mismatches 16; Indels
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                                                                      APPLICANT: Univers, march
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/245,410
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO S
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APPLICANT: McIntcah, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Scheenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Maren
APPLICANT: Schetty, Reshma
APPLICANT: SPECTY. Schema
APPLICANT: Walker, Craig
APPLICANT: W
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEC ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 570
LENGTH: 30
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McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.9%;
Matches 15; Conservative
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; ORGANISM: Hadronyche versuta
US-09-894-882-5
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ORGANISM: Conus lividus
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Best Local Similarity
Matches 13; Conserv
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CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32

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Gaps
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Pred. No. 1.1;
2; Mismatches 13;
APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: McInesh J, Michael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conctoxins FILE PETERBOOK: 214-238
CURRENT APPLICATION INVEST: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR APPLICATION NUMBER: US 60/29
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-7
PRIOR PILING DATE: 2000-11-08
                                                                                                                                                               APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF WINSMILL CONE Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR FILING DATE: 2001-02-09
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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SOFWARE: Patentin version 3.0
SEQ ID NO 137
LENGTH: 77
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Best Local Similarity 44.8%;
Matches 13; Conservative
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Walker, Craig S.
Shetty, Reshma
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; ORGANISM: Conus lividus
US-10-072-602B-137
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NAME/KEY: unsure
LOCATION: 2762, 2778
CHER INFORMATION: unknown base
US-10-123-155-37
Olivera, Baldomero M.
Watkins, Maren
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Stewart, Timothy A.
Tumas, Danial
Watanabe, Colin K
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Best Local Similarity 44.8%;
Matches 13; Conservative 2
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Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
Gao, Wei-Qiang
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; ORGANISM: Conus emaciatus
US-09-894-882-247
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FEATURE:
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0.7;
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35.6%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels
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Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Resha
APPLICANT: Malker, Craig S.
APPLICANT: Malker, Craig S.
APPLICANT: Malker, Chaig S.
APPLICANT: Malker, Malker, Chaig S.
APPLICANT: Malker, Chaig S.
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation
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APPLICANT: Warfins, waren
APPLICANT: Shen, Greg S.
TITLE OF INVENTIAON: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/243, 410
PRIOR APPLICATION NUMBER: US 60/243, 410
PRIOR APPLICATION NUMBER: US 60/243, 410
PRIOR PLING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247, 714
PRIOR APPLICATION NUMBER: US 60/247, 714
PRIOR APPLICATION NUMBER: US 60/247, 714
PRIOR APPLICATION NUMBER: US 60/264, 256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 497
LENGTH: 39
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                                                                                                                                                                                                                                                                    CPPPGIYCTPYLPCCWGICC--GTCRNVC 27
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 497, Application US/09894882 Patent No. US20020102607A1
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McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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Best Local Similarity 44.8%;
Matches 13; Conservative
        SOFTWARE: PatentIn version 3.0 SEQ ID NO 461 LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
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ORGANISM: Conus emaciatus
US-09-894-882-497
                                                                    TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333-0016.20
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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APPLICANT: Gross, Robert M.
APPLICANT: Shen, Greg S.
TILLE OF INVENTION: 1-Superfamily Conctoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-16-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PARCENTIN VERSION 3.0
SEQ ID NO 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Mood, William
APPLICANT: ACOUNT: ACOU
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TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT PPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
LENGTH: 3501
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Publication No. US20030148432A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
CCATION: 2762, 2778
CTHER INFORMATION: unknown base
US-10-140-472-37
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; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-141-761-37
                              Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary B.
Goddard, Audrey
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Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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Sherwood, Steven
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ORGANISM: Homo Sapien
FEATURE:
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT APPLICATION NUMBER: US/10/146,731
PRIOR Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 37
                                                                                                       Gaps
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                              Query Match 35.1%; Score 68; DB 14; Length 3501; Best Local Similarity 46.2%; Pred. No. 50; Matches 12; Conservative 0; Mismatches 14; Indels C
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Publication No. US20030138888A1
ENDICATON: BAKEr, Kevin P.
APPLICANT: Beresin, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
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1.OCATION: 2762, 2778
VOTHER INFORMATION: unknown base
VS-10-146-731-37
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Filvaroff, Ellen
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Gurney, Austin L.
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ORGANISM: Homo Sapien
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us-10-019-823b-2.rapb

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                        0; Gaps
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35.1%; Score 68; DB 14; Length 3501;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 14; Indels' (
                        14; Indels
Best Local Similarity 46.2%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches
                                                                                                                            888 daccaaagtaccaagccrdrgcrgg 913
                                                                          1 GKICTPAGVKCPAALPCCPGLRCIGG 26
                                                                                                                                                                                                                                          Sequence 37, Application US/10142885; Publication No. US20030157604A1; GENERAL INFORMATION:
APPLICANT: Barkr. Kevin P.
APPLICANT: Bereshin, Maureen APPLICANT: DeForge, Laura APPLICANT: Pilvaroff, Ellen APPLICANT: Filvaroff, Ellen APPLICANT: Gao, Wel-Qiang APPLICANT: Gao, Wel-Qiang APPLICANT: Gao, Wel-Qiang APPLICANT: Gerritsen, Mary E.
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ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 27762, 2778
COTHER INFORMATION: unknown base
US-10-142-885-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary E. Goddard, Audrey
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Search completed: October 28, 2004, 18:40:50 Job time : 4.0145 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 28, 2004, 17:52:12 ; Search time 4.51795 Seconds (without alignments) 4202.652 Million cell updates/sec Run on:

US-10-019-823B-2 194 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33 Title: Perfect score: Sequence:

550 L

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	P82227 hadronyche	P82226 hadronyche	Q9tvn1 conus livid	Q9uaa2 conus livid	conus 1	Q9uaa7 conus livid	Q9uab0 conus livid	-	8 hadron		Q9uaa5 conus livid			Q7pmf9 anopheles g	. snuos	conns	conus l	Q9tw08 conus livid	Q9uaa0 conus livid	conus 1	conns	couns	Q9uab2 conus livid	Q9bp93 conus ventr	P10079 strongyloce	Q946y8 hordeum vul		Q75wh6 macrothele		E	Bad13405 macrothel
ID	TXJA HADVE	TXJB HADVE	Q9TVV1	Q9UAA2	Q9UAA4	Q9UAA7	Q9UAB0	Q9UAB1	TXJC HADVE	Q9UAA3	Q9UAAS	Q9GPA5	TXC5_PHONI	Q7 PMF9	CXK_CONVR	Q9UAA9	Q9UAB3	Q9TW08	Q9UAA0	Q9UAA1	Q9UAA6	Q9UAA8	Q9UAB2	Q9BP93	FBP1_STRPU	Q946 <u>Y</u> 8	Q9BP85	Q75WH6	BAD13402	Q75WH3	BAD13405
Length DB	36 1			72 2			72 2	72 2	7		0	2524 2	m	Ŋ	7		71 2	71 2	71 2	71 2	71 2	_	_		4	_	0	7	77 2		77 2
% Query Match 1	42.3	40.7	37.6	37.6	37.6	37.6	37.6	37.6	37.4	37.1		37.1	36.3			35.1		33.5		33.5	m.	33.5		33.2	۳	32.5		ď.	ć.	31.7	31.7
Score	82	79	73	73	73	73	73	^	72.5	72	72	72	70.5	69.5	69	68	99	65	65	65	e S	65	65	64.5	64	63	62.5	62	62	61.5	61.5
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QefnuB candida gla Qec187 kluyveromyc	Q6tvp0 orf virus. Aar98305 orf virus	Q05790 saccharomyc P49013 strongyloce O9u3w8 drosophila	Q8t019 drosophila Q9vm97 drosophila 096884 drosophila	9	Q7x1q7 oryza sativ
Q6FNU8 Q6CL87	Q6TVP0 AAR98305	Q05790 FBP3_STRPU O9113W8	Q8T019 Q9VM97 096884	Q61Q50 AAH71562	Q7XLQ7
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4 4 4 4 0 0 0	0 0 0 0 0 0 0 0	570 570	1060	1317	1529
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28.6	# տ խ Դ տ տ -	w w c	4 4 4 0 H 0	4 4	45

# ALIGNMENTS

RESULT 1

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DŢ	30-MAY-2000		Creat	J)		
ď	30-MAY-2000	(Rel. 39,	Last	sequence update)	pdate)	
Ιď	05-JUL-2004	(Rel. 44,	Last a	annotation update	updat	(e)
DE	Janus-atracotoxin-Hvla (J-AcTx-Hvla)	toxin-Hv1	a (J-Ac	rx-Hvla).		
SO	Hadronyche versuta (Blue mountains funnel-web spider)	ersuta (B	lue mou	ntains fu	nnel-w	veb spider) (Atrax
SO	versutus).					
Ö	Eukaryota; M	etazoa; A	rthropo	da; Cheli	cerata	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Ö	Mygalomorpha	e; Hexath	elidae;	Hadronyc	he.	
XO	NCBI TaxID=6904;	904;		i		
RN	[1]					
RP	SEQUENCE.					
RC	TISSUE=Venom;					
RX	MEDLINE=20343014; PubMed=10881200;	3014; Pub	Med=108	31200;		
RA	Wang XH., Connor M.,	Connor M.	, Smith R.,		Maciejewski	ci M.W., Howden M.E.H.,
RA	Nicholson G.M., Christie M.J., King G.F.	M., Chris	tie M.J	., King G		
RT	"Discovery and characterization	nd charac	terizat	ion of a	귺	of insecticidal
RT	neurotoxins with a	with a ra	rare vicinal	nal disulfide	fide	bridge.";
RL	Nat. Struct.	Biol. 7:	505-513	Struct. Biol. 7:505-513(2000).		
ប្ជ	-:- FUNCTION	: Insecti	cidal n	eurotoxin		
ប្ដ	-1- SUBCELLU	SUBCELLULAR LOCATION: Secreted.	NON: Se	creted.		
ខ្ល	-!- TISSUE S	PECIFICIT	Y: Expre	essed by	the ve	TISSUE SPECIFICITY: Expressed by the venom gland.
DR	HSSP; P82228; 1DL0.	; 1DL0.				
Æ	Direct protein	in sequen	cing; N	sequencing; Neurotoxin; Toxin	; Toxi	'n.
F	DISULPID			By similarity	aritv.	
FT	DISULPID		22	By similarity	arity.	
FŢ	DISULFID		14		arity.	
Ţ	DISTRIBLE	16	33	By similarity	aritv.	
SOS		A; 3	85 MW;		60BFE9	997 CRC64;
O	Ouerv Match		42.3%;	Score 82;	; DB 1;	1; Length 36;
i ii	Best Local Simi	Similarity	51.5%;	Pred. No.	O	
Ма	17;	vat		1; Mismatches	r)	13; Indels 2; Gaps
ò	3 ICT	PAGVKCPAA	TPCCPGL	ICTPAGVKÇPAALPÇÇPGLRÇIGGVNNKV	VCR	33
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QQ	Z ICE	GADRECAAC	II.SACCACI	ICTGADRPCAACCPCCPGTSCQGPESNGVVYCR	^∨x ८.ĸ	4.1

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MEDLINE=9728955; PubMed=10359796;

Duda T.F. Jr., Palumbi S.R.;

Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";

Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).

Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR004214; Conotoxin; IEA.

Pfam; PF02950; Conotoxin; 1.
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89426;
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46.4%; Pred. No. 0.2;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 73; DB 2; Length 72;
Pred. No. 0.2;
4; Mismatches 9; Indels
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GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotexin.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Four-loop conotoxin LVVIA (Fragment).
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EMBL, AF089930, ADD48185.1;
EMBL, AF089931, ADD48186.1;
EMBL, AF089933, ADD48186.1;
EMBL, AF089941, ADD48188.1;
EMBL, AF089941, ADD48196.1;
EMBL, AF089943, ADD48196.1;
EMBL, AF089943, ADD48199.1;
EMBL, AF089944, ADD48199.1;
EMBL, AF089946, ADD48199.1;
EMBL, AF089949, ADD48200.1;
EMBL, AF089949, ADD48203.1;
EMBL, AF089950; ADD48203.1;
EMBL, AF089951, ADD48203.1;
EMBL, AF089951, ADD48203.1;
EMBL, AF089951, ADD48203.1;
EMBL, AF089953, ADD48206.1;
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nes 13; Conservative
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Pfam; PF02950; Conotoxin; 1.
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MEDILINE=99289555; Pubmed=10359796;

Duda T.F. Jr., Palumbi S.R.; Palumbi S.R.;

Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";

Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).

EMBL; AF089902; AAD4813.1; --

EMBL; AF089902; AAD48158.1; --
                                                                                       MEDLINE=20343014; PubMed=10881200; Maciejewski M.W., Howden M.E.H., Nang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H., Nicholson G.M., Christie M.J., King G.F.; Christie M.J., King G.F.; Christie M.J., Sking G.F.; Christie M.J., Christie M.J., Sking G.F.; Christian Characterization of a family of insecticidal neurotoxins with a rare vicinal disulfide bridge."; Nat. Struct. Biol. 7:805-513(2000).
-!-SUBCELLULAR LOCATION: Secreted.
-!-TISSUE SPECIFICITY: Expressed by the venom gland.
HSSP; P82228; IDLO.
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Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 79; DB 1; Length 36;
Pred. No. 0.021;
0; Mismatches 14; Indels
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin LVVIA (Four-loop conotoxin LVVIB)
                                                                                                                                                                                                                                                                                                         Direct protein sequencing; Neurotoxin; Toxin.
DISULFID 3 17 By similarity.
DISULFID 10 22 By similarity.
DISULFID 13 14 By similarity.
DISULFID 16 33 By similarity.
SEQUENCE 36 AA, 3651 MW; D23A442560B89997 CRC64;
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1 Similarity 51.5%;
17; Conservative
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AF089907; AAD48163.1;
AF089910; AAD48165.1;
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AAD48170.1
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         NCBI_TaxID=6904;
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ilarity 46.4%;
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Matches 13; Conserv
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EMBL; AR089912; AAA48167.1; -
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0008405; P:pathogenesis; IEA.
InterProc. 1PR004214; Conotoxin.
Pfam; PF02950, Conotoxin; 1.
                                                                                                                                                                                         MEDLINES FROM MAN DECEMBER 193996;
MEDLINES FROM MAN DECEMBER 1939986;
Muda T.F. Jr., Palumbi S.R.;
Molecular genetics of ecological diversification: duplication and rapid evolution of texin genes of the venomous gastropod Conus.";
Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).

EMBL; ARS09955; Ab1048210.1; -
EMG.; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conocoxin.
PF02950; Conocoxin; 1.
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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46.4%; Pred. No. 0.2;
tive 4; Mismatches 9; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                  Last sequence update)
Last annotation update)
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               01-MAY-2000 (TYEMBLrel. 13, Created) 01-MAY-2000 (TYEMBLrel. 13, Last seq 01-007-2003 (TYEMBLrel. 25, Last ann Four-loop conotoxin LVVIA (Fragment) conus lividus.
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EMBL; AF089904; AAD48160.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ton channel inhibitor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conctoxin.
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MEDLINE 92889555; pubMed=10359796;
Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";
Proc. Natl. Acad. Sci. U. S.A. 96:6820-6823 (1999).
EMBL; AF089905; AAD48161.1; -
GO; GO:0005506; C:extracellular; IEA.
GO; GO:000506; F:ion channel inhibitor activity; IEA.
GO; GO:000506; P:pathogenesis; IEA.
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Pred. No. 0.2;
4; Mismatches 9; Indels
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46.4%; Pred. No. 0.2;
tive 4; Mismatches 9; Indels
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                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Four-loop conotoxin LVVIA (Fragment).
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72 AA
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Duda T.F. Jr., Palumbi S.R.;
Molecular genetics of ecological diversification: duplication and
rapid evolution of toxin genes of the venomous gastropod Conus.";
Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Hadronyche.
Mygal_TaxID=6904;
                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                    Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72.5; DB 1; Length 37;
Pred. No. 0.13;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E4DDF046CC750FFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Four-loop conotoxin LVVIA (Fragment).
                                                                                                                                                                  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 45, Last amotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          icigadrecaacceccecrasckaesugvsyck 33
                                                                                                                                   37 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR
2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
                                  42 RTCSPAGEVCTSKSPCCTGFLCSHIGGM 69
                                                                                                                                                                                                                                    Janus-atracotoxin-Hv1c (J-AcTx-Hv1c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.4%;
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
01-OCT-2004 (Rel. 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=89426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus lividus
                                                                                                                                   HADVE
                                                                                                                                                                                                                                                                         versutus)
                                                                                                                                                                                                                                                                                                                                                                   SEOUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
                                                                                                          TXJC_HADVE
IID _TXJC_HADVE
IID _30-MAY.
DT _31-MAY.
DT _31-MAY.
DE _Janus.
OS _Werry
OS _Werry
OC _ Eukaryt
OC _ Eukaryt
OC _ Mygalo
OC _ Mygalo
OC _ Mygalo
OC _ Mygalo
OC _ Hygalo
OC _ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAND
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090AA
AC 090AA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MC
DE FOUR-
OC APOGA
OC APOGA
OC NGBI
RN (1)
RA SEQUE
RA DUMA
RT "MOIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Branchiostoma floridae (Florida lancelet) (Amphioxus).
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCNI_TaxID=89426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A.
IISSUE=Whole larvae;
Holland L.Z., Burgtorf C., Holland N.D., Lehrach H., Tamme R.,
                                                                                                                                              Length 72;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
GO; GO:0005576; C:extraceliular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
Pfam, PF02950; Conotoxin, 1.
SEQÜENCE 72 AA; 8014 MW; C2757DDC87553EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AA; 7915 MW; D9757DCD87553EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 37.1%; Score 72; DB 2; Local Similarity 50.0%; Pred. No. 0.27; es 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 2;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                 72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                      4 CTPAGVKCPAALPCCPGLRC--IGGV 27
                                                                                                                                                                                                                                                       44 CSPAGEVCTSKSPCCTGFLCSHIGGM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CTPAGVKCPAALPCCPGLRC--IGGV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 CSPAGEVCTSKSPCCTGFLCSHIGGM 69
                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Created) 01-WAY-2000 (TrEMBLrel. 13, Last seqnoror-2003 (TrEMBLrel. 25, Last and Four-loop conotoxin LVVIA (Fragment) conus lividus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Gaps

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Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
nigriventer has sequence similarities with snake disintegrins, vasococin-neurophysins and other spider toxins.";
Submitted (JUN-2004): to Swiss-Prot.
-!- FUNCTION: Non-toxic to mice.
-!- FUNCTION: Non-toxic to mice.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECIFICITY: MW=3672.7; METHOD=Electrospray; RANGE=1-33; NOTE-Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=PEST;
Anophales Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 3775;
                                                                                                                                                                                                                         Score 70.5; DB 1; Length 33;
Pred. No. 0.2;
6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3775 AA; 396198 MW; 51C4106F6E9908F4 CRC64;
                                                                                                                                                                   Direct protein sequencing. SEQUENCE 33 AA, 3679 MW; 77F1127D4785D6E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP00000011881 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMEL, AAABOLO08960; EAA13897.2; -...

GO; GO:0005509; F:calcium ion binding; IEA.

InterPro; IPRO00152; Asx hydroxyl_S.

InterPro; IPRO01891; BGF Z.

InterPro; IPRO01801; BGF Z.

InterPro; IPRO01801; BGF Z.

PF MM: PPO0008; EGF Z.

PF MM: PPO0008; EGF Z.

PROSITE; PS00010; ASX HYDROXYL; 17.

PROSITE; PS00010; CTYPE LECTIN I, UNKNOWN I.

PROSITE; PS00025; EGF Z.

PROSITE; PS00186; EGF Z.

PROSITE; PS01186; EGF Z.

PROSITE; PS01186; EGF Z.

PROSITE; PS01187; EGF Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ICT-PAGVKCPAALPCCPGLRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 3775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.8%; Score 69.5; D
Best Local Similarity 41.9%; Pred. No. 18;
Matches 13; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                        4 CTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
                                                                                                                                                                                                                                                                                                                                  3 CAQKGIKC-HDIHCCTNLKCVREGSNRVCR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Created)
                                                                                                                                                                                                                             36.3%;
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Best Local Similarity 40.0°
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ENSANGG00000009392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=180454;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
07PMF9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richardson M., Pimenta A.M.C., Bemquerer M.P., Santoro M.M., Figueiredo S.G., Cordeiro M.N., "New peptide PN10C5 from venom of Brazilian armed spider Phoneutria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phoneutria nigriventer (Brazilian armed spider).
Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Araneomorphae, Entelegynae, Lycosoidea, Ctenidae, Phoneutria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.1%; Score 72; DB 2; Length 2524; 45.9%; Pred. No. 6.3; tive 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00004; NL; 3.

PROSITE; PSS0089; ANK_REPEAT; 4.

PROSITE; PSS0019; ANK_REP REGION; 1.

PROSITE; PS00100; ASK_HYDROXL; 23.

PROSITE; PS00120; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01187; EGF_3; 36.

PROSITE; PS01187; EGF_3; 36.

ANK_REPEAT; BGF-11ke Gomain; Receptor.

SEQUENCE 2524 AA; 270970 WW; C2CA57E306D23EC9 CRC64;
        rotti P., Lardelli M.;
to the EMBL/GenBank/DDBJ databases.
                                                                    SEQUENCE FROM N.A.
TISSUB-Whole larvae;
Lardelli M.T.;
Submitted (AFR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   768 CLPGYEGVNCDINTDECASNPCQNGGRCLDGVNNYVC 804
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01-0CT-2004 (Rel. 45, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Venom protein PN10C5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 AA.
                                                                                                                                                                                      GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:recalcium ton binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
                                                                                                                                                                                                                                                                    InterPro; IPR002110; ANK.
InterPro; IPR000110; Ank.
InterPro; IPR000182; Ask hydroxyl S.
InterPro; IPR000895; Cond like leg_gl.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR000143; EGF_2.
InterPro; IPR001801; EGF_II.
InterPro; IPR001801; EGF_II.
InterPro; IPR000800; NOD.
InterPro; IPR000800; NOD.
InterPro; IPR000800; NOD.
          Abi-Rached L., Pontarotti P.,
Submitted (APR-1997) to the EN
                                                                                                                                                  EMBL; Y12539; CAC19873.1; -. HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00248; ANK; 6.
SMART; SM00179; EGF CA; 21.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PP00023; Ank; 6.
Pfam; PP00009; EGF; 34.
Pfam; PP07645; EGF_CA; 2.
Pfam; PP06816; NOD; 1.
Pfam; PP00066; Nocch; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1415; ANKYRIN.
PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 45.9
Matches 17, Conservative

    STANDARD;

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TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TXC5_PHONI
ID _TXC5_PHONI
AC P84015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij,
                                                                                                                                                                                                                                                                                                                                                                                 12SUBERTON N.A.
TISSUBE-Venom duct;

Kauferstein S.;

Thesis (2001), University of Darmstadt, Germany.

-! FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive potassium channels. This toxin inhibits the vertebrate potassium channels KV1.1 and KV1.3, but not KV1.2. It has no effect on HERG-type channels sodium hH1 channels and Kir-type channels (IRK1).
-! SUBELLIUIAR LOCATION: Secreted.
-! TISSUB SPECIFICITY: Expressed by the venom duct.
-! PTM: Contains four disulfide bonds.
-! PTM: Contains four disulfide bonds.
                                                                                                                                                                                                                                                                                   PubMed=12893060;
Kanicestein S., Huys I., Lamthanh H., Stocklin R., Sotto F., Menez A.,
Tyrgat J. Mebs D.;
"A novel conotoxin inhibiting vertebrate voltage-sensitive potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE-Ref.1. SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
                                                                                                              Conus virgo (Virgin cone).

Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.6%; Score 69; DB 1; Length 67; llarity 44.8%; Pred. No. 0.57; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P -> S (in Ref. 1).
G -> S (in Ref. 1).
46671D012446F62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kappa-conotoxin ViTx.
                        29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
805-JUL-2004 (Rel. 44, Last annotation update)
Kappa-conotoxin Virx precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct protein sequencing; Signal; Toxin. SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                   PRT;
                                                                                                                                                                                                                                                   SPECTROMETRY.
TISSUE=Venom, and Venom duct;
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49
7599 MW;
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                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AA;
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                   CONVR
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Matches
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29 CFPPGIYCTPYLPCCWGICC--GTCRNVC 55

Search completed: October 28, 2004, 18:29:44 Job time : 6.6608 secs

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Sequence 497, App
Sequence 274, App
Sequence 478, App
Sequence 274, App
Sequence 28474, App
Sequence 16, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 248, Appli
Sequence 286, Appli
Sequence 2386, Appli
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                                                               October 28, 2004, 18:06:07; Search time 1.02508 Seconds (without alignments) 2134.948 Million cell updates/sec
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Sequence 6,
Sequence 6,
Sequence 5,
Sequence 5,
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(cgn2_6/ptodata1/liaa/5A_COMB.pep:*
(cgn2_6/ptodata1/liaa/5B_COMB.pep:*
(cgn2_6/ptodata1/liaa/6A_COMB.pep:*
(cgn2_6/ptodata1/liaa/6B_COMB.pep:*
(cgn2_6/ptodata1/liaa/6B_COMB.pep:*
(cgn2_6/ptodata1/liaa/pcTUS_COMB.pep:*
(cgn2_6/ptodata1/liaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-894-882-4

US-08-682-485A-7

US-08-682-445A-6

US-08-893-314-6

US-09-894-882-497

US-09-894-882-497

US-09-894-882-497

US-09-894-882-497

US-09-894-882-497

US-09-894-882-497

US-09-894-882-498

US-08-913-11

US-08-913-11

US-08-913-1445-1

US-08-914-144

US-08-914-144-5

US-08-914-741-44
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1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33
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US-09-510-238A-286
US-09-252-991A-23962
US-09-907-794A-109
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB seq
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No.
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    109, App
109, App
290, App
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111, App
111, App
11692, A
296, App
502, App
502, App
502, App
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502, App
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                   US-09-902-775A-109
US-09-902-775A-109
US-09-906-700-109
US-09-906-700-109
US-09-903-603A-109
US-09-101-241-11
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Pred. No. 0.004;
1; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-00-894-882-3
Sequence 3, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. 6767895
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Best Local Similarity 51.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ; ORGANISM: Hadronyche versuta US-09-894-882-3
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GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 36;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPRANE: PETENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

38.7%; Score 75; DB 1;

Best Local Similarity 50.0%; Pred. No. 0.026;

Matches 16; Conservative 0; Mismatches 1
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                                                                                                                  FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Mellissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: 38,301
REFERENCE/DOCKET NUMBER: 9PD 5099/D1
REFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-UUX-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-UUX-1994
APPLICATION NUMBER: W0 93/15108
FILING DATE: 29-DAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-OAN-1993
ATTORNEY AGENT INFORMATION:
NAME: Shaw, Melissa A.
US/08/256,933
                                                                       UMBER: WO 93/15108
29-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Zeneca, Inc.
1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
                                      FILLING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Austral 1200 C. CITY: Richmond
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STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-682-485A-7
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US-08-933-314-7
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APPLICANT: ATKINSON, RONALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: TYLER, MARGARET I
TILE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Punnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 40.7%; Score 79; DB 4; Length 36; Best Local Similarity 51.5%; Pred. No. 0.009; Matches 17; Conservative 0; Mismatches 14; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
                                                    University of Utah Research Foundation
                                                                                          APPLICANT: COGNETIX, INC.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Olones, Elsie C.
APPLICANT: Mointosh, J. Michael
APPLICANT: Mointosh, J. Michael
APPLICANT: Olones, Robert M.
APPLICANT: Sheet M.
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/245,811
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-18
SEQ ID NOS: 506
SEQ ID NOS
SEQ ID NOS
SEQ ID NOS
LENGTHR. 36
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 n v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-UULY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08682485A Patent No. 5763568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Hadronyche versuta
US-09-894-882-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-682-485A-7
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Gaps 7

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OTHER INFORMATION: /label= a OTHER INFORMATION: /note= "this site may be amidated without loss OTHER INFORMATION: of biological activity"
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APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONNEX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEGUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.7%; Score 75; DB 1; Length 37; Best Local Similarity 50.0%; Pred. No. 0.027; Matches 16; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/933,314
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-196
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 32-JAN-1993
APPLICATION NUMBER: MU PLO722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
RESERBATION NUMBER: PPD 5099/D1
REJERPONE: ALORAMATION:
TELEPHONE: S10-231-11-542
TELEPHONE: S10-231-11-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CIPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08933314
Patent No. 5959182
GENERAL INFORMATION:
                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site LOCATION: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510-231-1112
                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                      2
                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-682-485A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-933-314-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequent No. 576358

Parent No. 576358

GENERAL INFORMATION:
APPLICANT: HOWDEN, RONALD K
APPLICANT: HOWDEN, MELLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD T
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 2
CORRESSEB: Zeneca, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 2; Length 36;
Pred. No. 0.026;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTROL OF THE CASE THE CATION NUMBER: US/08/682,485 FILING DATE: US/08/526,933 FILING DATE: US/08/56,933 FILING DATE: US/08/56,933 FILING DATE: US/08/56,933 FILING DATE: US/08/266,933 FILING US/08/266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CTGADRPCAACCPCCPGTSCKGPEPNGVSYCR 35
                                               PPD 5099/D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Zeneca, Inc.
1200 South 47th Street
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
US-08-933-314-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 510-231-1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.7%;
Best Local Similarity 50.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1200 South
CITY: Richmond
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-682-485A-6
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University of Utah Research Foundation
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                                                                                                                                                                                                          LOCATION: 37
COTHER INFORMATION: /label= a
OTHER INFORMATION: /note= "this site may be amidated without loss
OTHER INFORMATION: of biological activity"
US-08-933-314-6
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERĀL INFORMATION:
APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.7%; Score 75; DB 2; Best Local Similarity 50.0%; Pred. No. 0.027; Matches 16; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OHIVETALLY INC.
APPLICANT: Shelty, Reshma
APPLICANT: Shelty, Reshma
APPLICANT: Shelty, Reshma
APPLICANT: Shelty, Reshma
APPLICANT: Matters, Baldomero M.
APPLICANT: Mattins, Maren
APPLICANT: Matkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: DATE: 2001-06-29
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICANTION NUMBER: US 60/246,581
PRIOR APPLICANTION NUMBER: US 60/246,581
PRIOR PLING DATE: 2000-11-14
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 icigadrecadcepceperschaesngvsyck 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 craadrecadececestscherengister 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09894882
Patent No. 6767895
                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Atrax formidabilis
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-5
                                                                                                                                                                                     NAME/KEY: Modified-site
               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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Sequence 461, Application US/09894882 Patent No. 6767895 GENERAL INFORMATION:

RESULT 8 US-09-894-882-461

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Gaps
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Sherty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
FURRENT Shen, Greg S.
TITLE OF INVENTION UNMERS: US 60/244,882
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                 AFPLICATION STANDARY 
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35.6%; Score 69; DB .
Best Local Similarity 44.8%; Pred. No. 0.12.
Matches 13; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFPPGIYCTPYLPCCWGICC--GTCRNVC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
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Patent No. 6767895
GENERAL INFORMATION:
Walker, Craig S.
Shetty, Reshma
Jimenez, Bisle C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Conus emaciatus
US-09-894-882-461
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US-09-894-882-497
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JOILES, ACCELT.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE PAREITY NOWERE: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE PAREITY VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marten, APPLICANT: ARTEN, APPLICANT: Shen, Greg S.

ITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US,09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR FILING DATE: 2000-16-27

PRIOR FILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: US 60/245,581

PRIOR PLING DATE: 2000-11-04

PRIOR APPLICATION NUMBER: US 60/247,714

PRIOR PLING DATE: 2000-11-14

PRIOR FILING DATE: 2001-10-29

NUMBER OF SEQ ID NOS: 506

SOFTWARE: PARCELLING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 506

SEQ ID NO 498

LENGTH: 40
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Pred. No. 0.25,
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CTPAGVKCPAALPCCPGLRCIG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFPLGTFCSRYLPCCSGMCCSG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
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50.0%;
                 Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Conus virgo
US-09-894-882-470
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, ORGANISM: Conus virgo
US-09-894-882-498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                    Query Match 35.6%; Score 69; DB 4; Length 39; Best Local Similarity 44.8%; Pred. No. 0.14; Matches 13; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 470, Application US/09894882
Patent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Malker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIncosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Matkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Waterlas, waren
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-2 Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION INDER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/209
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-34
PRIOR FILING DATE: 2000-11-34
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2001-11-3
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PARCHELL VOS: 506
SOFTWARE: PARCHELL VOS: 506
SED ID NO 247
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB 4;
Pred. No. 0.23;
2; Mismatches
                                                                                                                                                                                                                                 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPPPGIYCTPYLPCCWGICC--GTCRNVC 55
                                                                                                                                                                                                                                                                               1 CFPPGIYCTPYLPCCWGICC--GICRNVC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                                                                                                                           US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
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Best Local Similarity 44.8
Matches 13; Conservative
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ; ORGANISM: Conus emaciatus US-09-894-882-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-894-882-470
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Gaps

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Sequence 16, Application US/08185432

Patent No. 5750652

GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Busseau, Isabelle
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTER PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES:
ADDRESSE:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CORRESPONDENCE PENNIE & EDWONDS
                                                              ;
0
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Score 59; DB 4; Length 155; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-271
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILLING DATE: 21-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ICTP--AGVKCP-----AALPCCPGLRCIGGVNNKVC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.4%; Score 59; DB 1; Best Local Similarity 36.8%; Pred. No. 94; Matches 14; Conservative 4; Mismatches 12
                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: October 28, 2004, 18:34:07 Job time : 3.02508 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-
TELECHOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAK: (212) 869-8664/9741
                                                                                                                       5 TPAGVKCPAALPCCPGLRC 23
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 52.6%;
Matches 10; Conservative
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APPLICANT: MACCHAILOW:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-118

FULE REPERENCE: 107196-118

FULE REPERENCE: 107196-118

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.5%; Score 67; DB 4; Length 68; 50.0%; Pred. No. 0.41; ive 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                        GENERAL NO. 676 893

GENERAL NO. 676 893

GENERAL NO. 676 893

APPLICANT: University of Utah Research Foundation
APPLICANT: Walker, Cane 1.

APPLICANT: Walker, Inc.

APPLICANT: Walker, Inc.

APPLICANT: Shetty, Reshma
APPLICANT: March 1.

APPLICANT: Markins, Maren
APPLICANT: Olivera, Baldomero M.

APPLICANT: Olivera, Baldomero M.

APPLICANT: Olivera, Baldomero M.

APPLICANT: Shen, Greg S.

TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 2314 -238

CURRENT FILING DATE: 2000-06-29

FRICR APPLICATION NUMBER: US 60/246, 581

FRICR PILING DATE: 2000-11-28

FRICR FILING DATE: 2000-11-27

FRICR FILING DATE: 2000-11-48

FRICR FILING DATE: 2000-11-44

FRICR FILING DATE: 2000-11-14

FRICR FILING DATE: 2000-11-14

FRICR APPLICATION NUMBER: US 60/247, 714

FRICR PILING DATE: 2000-11-14

FRICR FILING DATE: 2000-11-14

FRICR PILING DATE: 2001-11-14

FRICR FILING DATE: 2001-11-14
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; Sequence 28474, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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             CTPAGVKCPAALPCCPGLRCIG 25
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28474
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CORGANISM: Conus virgo
US-09-894-882-274
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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SUMMARIES	ΩĦ	AAB66907	AAE36271	AAR08041	AAU02095	AAB66909	AAE36273	AAB66908	AAE36272	AAB66910	AAE36274	AAB66911	AAE36275	ADM74717	AAB66912	AAE36276	AAU02041	ABB07073	AAW49089	AAU02092	AAU02093	ADK98484	ADK98489	ADK98481	ADK98491	ADK98487
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	Query Match Length	718	718	719	719	719	719	719	719	719	719	719	719	719	719	719	710	719	719	1217	1208	1230	1230	1230	1230	1230
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## ALIGNMENTS

The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB6689) to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production. Warner SAJ; Insecticide; transgenic plant; insect-resistance. Mackay EA, Cayley PJ, Claim 14; Page 53-55; 72pp; English. AAB66907 standard; protein; 718 AA. 99GB-00015215. 23-JUN-2000; 2000WO-GB002457. Insecticidal protein cryllal. (first entry) Griffin J, Carlile AJ, Vincent JL, Lee MD; WPI; 2001-123015/13. (ZENE ) ZENECA LTD. Sequence 718 AA; WO200100841-A1. 29-JUN-1999; 23-DEC-1999; Paecilomyces 12-APR-2001 04-JAN-2001. AAB66907; 

Query Match 99,93; Score 3747; DB 4; Length 718;
Best Local Similarity 100.03; Pred. No. 9e-296;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 717; Conserv
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                                QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA
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                                                                                                                                                                                                                                                                                                                                                             pesticide; insecticidal crystal endotoxin;
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                                                                                                                            The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crivity. The present sequence is sequence is used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGHKLEFRTIGGTLNISTQGSTWTSINDVTLPFTSRDVYRTESLAGLNLFLTQPVWVPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHVKALVYSWTHRSADRIVTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FXTVGFTTPPSLLDVQSTFT1GAWNFSSGNEVYIDR1EFVPVEVTYEAEYDFEKAQEKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3747; DB 6;
Pred. No. 9e-296;
0; Mismatches 1
                                                                                      Claim 12; Page 42-44; 67pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.9%;
ilarity 99.9%;
Conservative C
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419 420 479 480 539 540

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Crystal protein; CrylIa; CrylBa; moth; butterfly; Colorado potato beetle; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                                                                                                                                                                                                                                    TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
GTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVIISSLLSRWSNIQYMMW
                                                                                                                    421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                481 ASHVXALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
                                                                                                                                                                                                                  540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                      361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                   VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                            ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                                                                                                           600 TEXTVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                          361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
                                                                                                                                                                                                                                                                                                     601 TEXTVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is B. thuringiensis (Bt) crystal protein Crylla, the DNA encoding which was mutated to allow cloning of domain III or domains
                                                                                                                                                                                                                                                                                                                                   TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKOLHIERNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis partial mutant Crylla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20. 719
/label= Mature_CrylIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02095 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosch HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-337141/36.
N-PSDB; AAS04855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Maagd RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1099760-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1999;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence carried on pJH12 which was isolated from B. thurin- giensis strains JHCC4835 and JHCC 4353 (NGIB 40091 and 40090 resp.). The DNA can be used to produce transformants B.coli strain MC12022/pJH12 (NCIB 40278) or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-WAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEBIINQKISTYA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                       81 kD endotoxin deduced from DNA carried on pJH12
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.7%; Score 3736.5; DB 2
99.9%; Pred. No. 6.4e-295;
ive 0; Mismatches 0;
                                                                                                                                                                                     delta endotoxin.
                                                                                                                                                                                                               Bacillus thuringiensis; JHCC 4353 and 4835
                                                                                                                                                                                                                                                                                                                                                                                         Tippett JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 5-10; 66pp; English
                                      AAR08041 standard; protein; 719
                                                                                                                                                                                                                                                                                                                                                                                         Tailor RH,
                                                                                                                                                                                                                                                                                                                                                          (ICIL ) IMPERIAL CHEM IND PLC
                                                                                                                                                                                                                                                                                                                                89GB-00010624.
                                                                                                                                                                                   Crystal; insecticide; toxin;
                                                                                                                                                                                                                                                                                                     89GB-00010624
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.9
                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-361486/48.
                                                                                                                                                                                                                                                                                                                                                                                         Ely S,
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ06636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 719 AA;
                                                                                               24-OCT-2003
25-MAR-2003
27-FEB-1991
                                                                                                                                                                                                                                                                                                   09-MAY-1989;
                                                                                                                                                                                                                                                                                                                                09-MAY-1989;
                                                                                                                                                                                                                                            WO9013651-A.
                                                                                                                                                                                                                                                                         15-NOV-1990.
                                                                                                                                                                                                                                                                                                                                                                                         Blenk RG,
                                                                     AAR08041;
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Matches
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SAJ;

Warner

Mackay EA,

PJ,

Cayley

99GB-00015215.

2000WO-GB002457

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Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant
                                                                                                                                                                                                          Claim 14; Page 57-59; 72pp; English
                                                                                                                       Carlile AJ,
Lee MD;
                                                                                                                                                   WPI; 2001-123015/13.
                                                                                                      (ZENE ) ZENECA
                  WO200100841-A1.
 Paecilomyces
                                                       23-JUN-2000;
                                                                         29-JUN-1999;
                                                                                                                        Griffin J,
Vincent JL,
                                      04-JAN-2001
                                                                                                                                                                                        production.
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and II, to make the hybrid protoxins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
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                                                                           Score 3732.5; DB 4;
Pred. No. 1.4e-294;
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16; Conservative
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The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66895 to AAB66901 and AAB6691). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant, Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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                                                                                                                                                    Score 3724.5; DB 4;
Pred. No. 6.1e-294;
1; Mismatches 3;
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Best Local Similarity 99.3%;
Matches 714; Conservative
                                                                                                                        Sequence 719 AA;
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Insecticide; transgenic plant; insect-resistance

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TALFITSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB66908 standard; protein; 719 AA
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99GB-00030536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal activity. The present sequence is sequence is used in the invention
TRXTVGFTTPFSLLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 659
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                                                                                                                            TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
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                                                                                                                                                                                                                                                                                                                                                                                                  Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insecticidal protein comprising an X-glycine motif at terminus, useful as an active ingredient of a pesticide.
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Pred. No. 6.1e-294;
1; Mismatches 3;
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The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB6691 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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Pred. No. 8.9e-294;
); Mismatches 3;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiansis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
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Best Local Similarity 99.4%;
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(first entry)

26-JUN-2003

AAE36272 ID AAE3 XX AC AAE3 XX DT 26-J XX XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TALFTSINPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFELVKYAKQLHIERNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; pesticide; insecticidal crystal endotoxin; CRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. thuringiensis insecticidal crystal endotoxin (CRY) protein,
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terminus, useful as an active ingredient of a pesticide.
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                                                                          RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                        TEXTVGFTTPPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant production.
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                                                                                                                                                                                                                                                                                                                                         Insecticide; transgenic plant; insect-resistance.
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                                                                                                                                                                                                                                                                                                                                                                     Paecilomyces sp.
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Vincent JL,
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Matches
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Warner SAJ;

EA,

Mackay

Ρ.

Cayley

Carlile AJ, Lee MD,

Griffin J, Vincent JL,

(ZENE ) ZENECA LTD

WPI; 2001-123015/13

99GB-00015215 99GB-00030536

29-JUN-1999; 23-DEC-1999;

23-JUN-2000; 2000WO-GB002457

Paecilomyces sp. WO200100841-A1 Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant

Claim 14; Page 62-64; 72pp; English

production

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resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
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Pred. No. 1.9e-293;
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Best Local Similarity 99.3
Matches 714; Conservative
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Insecticide; transgenic plant; insect-resistance

protein cryllas

Insecticidal

12-APR-2001

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protein;

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AAB66911

AAB66911

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TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
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                                                                                                                                                                      TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDBKRELFEIVKYANELHIERNM 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; pesticide; insecticidal crystal endotoxin; CRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insecticidal protein comprising an X-glycine motif at the aminoterminus, useful as an active ingredient of a pesticide.
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Pred. No. 7e-293;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       thuringiensis insecticidal crystal endotoxin (CRY)
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                                                                                                                                                                                                                                                                                      AAE36275 standard; protein; 719 AA
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Best Local Similarity 99.0'
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                                          BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                       VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                           TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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with high-toxicity to lepidoptera pests, encoded protein, primer
sequences and the shuttle vector pSXX422b, useful as a pesticide
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N-PSDB; ADM74716.
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Insecticide; transgenic plant; insect-resistance.

protein cryllbl

Insecticidal

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                          combination, expression vector, nucleotide sequence of the B thuringiansis cryl gene with high-toxicity to lepidoptera pests and the amino acid sequence of the protein encoded by it, cooperative use of the cryl gene with the expression product of crylAb or crylBa, primer sequences for expressing the genes, and the constructed shuttle vector pSXY42D. The gene in combination with the crylAb or crylBa genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the cryllel protein.
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           novel Bacillus thuringiensis cryl gene, gene
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              invention relates to a
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for

SAJ;

Warner

EA,

Mackay

РЛ,

Cayley

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Carlile

Griffin J, Vincent JL,

(ZENE ) ZENECA LTD

WPI; 2001-123015/13.

99GB-00015215.

2000WO-GB002457

23-JUN-2000; 29-JUN-1999; 23-DEC-1999;

04-JAN-2001

WO200100841-A1

Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant

Claim 14; Page 64-66; 72pp; English

production

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                                                                                                                                                                                                                                                                                                          The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKALSDLRGLGDALAVYHESLESWVENRNYTRARSVVKNQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFWEHVEEIINQKILTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
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Best Local Similarity 92.4%
Matches 664; Conservative
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AAB66912 standard;

RESULT 14

12-APR-2001

AAB66912

AAB66912 ID AAB6 XX AC AAB6 XX DT 12-A

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TGLINNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI GTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW

RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180

121

RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
                                                           599
                                                                                TGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
                                                                                                                      TRXIVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 659
                                                                                                                                        ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
                                                                                                                                                                                TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718

    B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryllb1.

                                                           TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                                                                                                                  Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
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larity 92.4%; Pred. No. 3.1e-274;
Conservative 31; Mismatches 23;
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                                                                                                                                                                                                                                                                                           standard; protein; 719
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vincent JL, Viner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA LTD
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OTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA 120 QTGIGIAGKILGTIGUPFAGQIASLYSFILGELWPKGKSQWEIFWEHVEEIINQKILTYA 120

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1 MKLKNPDKHQSLSSNAKVDKIATDSLKNFTDIELKNMNNEDYLRMSEHESIDPFVSASTI 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI

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Gaps

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23; Indels

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                                                                                                                   TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719
TEXTVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                             601 TERTIGETTERSEDVQSTETIGAMNESSGNEVYIDRIBEVEVEVTYBABEYDFEKAQBKV
                                                                                           TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
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421 VDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480

ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK

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GCHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 361 GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
3604.811 Million cell updates/sec

Title:
Perfect score: 3749
Sequence: 1 MKLKNODKHQSFSSNAKVDK......KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

lse : DIR 79:\* )
2: pirl:\* 2: pirls\* 3: pirls\* 4;: pirl\* 4;:

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S32647	S11446	JC7140	S32689	140589	A49785	USBSXH	A27323	S10228	I39811	JH0261	S11445	S19306	USBS8I	B29838	I39870
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## ALIGNMENTS

# 2	RESULT 1 Sparson orystal protein cryllal - Bacillus thuringiensis parasporal crystal protein cryllal - Bacillus thuringiensis NAlternate names: delta-endotoxin; parasporal crystal protein cryv NAlternate names: delta-endotoxin; parasporal crystal protein cryv Cipecies: Bacillus thuringiensis CiDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004 CiAccession: S25383 Miscropicol. 6, 1211-1217, 1992 Anithe: Identification and characterization of a novel Bacillus thuringiensis delta-endo Anithe: Identification and characterization of a novel Bacillus thuringiensis delta-endo Anithe: DNA Ancession: S25383 Anithe: DNA Ancession: S25383 Anithe: MD: S25833 Anithe: MD: MD: S25833 Anithe: MD: MD: MD: MD: MD: MD: MD: MD: MD: MD
	Query Match  99.6%; Score 3732.5; DB 2; Length 719; Best Local Similarity 99.6%; Pred, No. 2.2e-250; Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
do ob	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSBYENVEPPVSASTI 60
oy du	61 QTGIGIAGKILGTLGVPFAGOVASIYSFILGELWPKGKNOWEIFMEHVEEIINQKISTYA 120 61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA 120
25 G	121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
	181 EEVPLLPIYAQAANLHLLLKADASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240 181 EEVPLLPIYAQAANLHLLLKADASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240
\$ 8	241 TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFBSYDTOWYPIKTTAQLTREVYTDAI 300 141 TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFFSYDTOWYPIKTTAQLTREVYTDAI 300
δ da	301 GTVHPHPSFTSTTWYNNAPSFSA1EAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNW 360
95 DP	361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419 1

Qy 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 479 	QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539	Qy 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWRGEDLDYK 599 	Qy 600 TEXTVGETTPESLLDVQSTFTIGAWNFSSCNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 659 	Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718 	RESELT 3 INSECTED 19915.  INSECTED 19915.  C. Date 1992 201-1996 #text_change 09-Jul-2004 C. Date 1992 201-1996 #text_change 09-Jul-2004 C. Date 1992 201-19915 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004 C. Date 1992 201-19915 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004 C. Accession 19915 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004 C. Accession 19915 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004 A. Microbiol 29 19 19 10 10 10 10 10 10 10 10 10 10 10 10 10	
Qy 420 UDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 479	QY 480 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSCAAVVRGPGFTGGDILRRTN 539	CY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATWRGEDLDYK 599	Qy 600 TFXTVGFTTPPFSLLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEABYDFEKAQEKV 659	Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEPYLDEKRELFEIVKYAKQLHIERNM 718 	RESULT 2 Insecticidal protein cryv1 - Bacillus thuringiensis Insecticidal protein cryv1 - Bacillus thuringiensis Insecticidal protein cryv1 - Bacillus thuringiensis Chaese 13-dung 84 = 8 edgenero= cryv1 - 8	

CY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 479	OY 420 VDFHWKFVTHPIASDNFYYEGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 479
QY 480 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN 539	Oy 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVROPGFTGGDILRRIN 539  481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN 540
QY 540 IGTFGDIRVNINPPFAQRYRVRIRYASTIDLOFHTSINGKAINQGNFSAIMRGEDLDYK 599	Qy 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 599
QY 600 TEXTVGFTTPPSLLDVQSTFTIGAMNFSSGNBVYIDRIEFVPVBVTYEABYDFBKAQEKV 659	Qy 600 TPXTVGFTTPFSLLDVQSTFTIGAMNFSSGNEVXIDRIEFVPUBVTYEAEYDFEKAQEKV 659
QY         660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYÄKQLHIERNM 718           DD         661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYÄKQLHIERNM 719	Qy 660 TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718 
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Cy 428 THPIASDNFYYPGYACIGTOLODSENELPPEATGQPNYESYSHRLSHIGLISASH 482	thuringi
QY 483 VKALVYSWTHRSADRTWIIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGDILRRINTGT 542	C.; Saey, B.; Seurinck, J
FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWARGEDLDYKTFX	A,Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agair A,Reference number: A59350, MUID:96141404, PMID:8572715 A,Accession: A59350 A,Accession: A59350 A,Accession: A59350
603 TVGFTTPFSLLDVQSTFTIGAWNFSSGNBVYIDRIEFVPVEVTYBAEYDFEKAQEKVTAL        :	A)Residues: 1-1157 <lam> A)Residues: 1-1157 <lam> A)Cross-references: UNIPPOT: 045733; EMBL: Z37527; NID: g547554; PIDN: CAA85764.1; PID: g54755 A)Experimental source: serovar tolworthi C; Comment: This parasporal crystal protein, active against corn borer and other insects, C; Superfamily: parasporal crystal protein</lam></lam>
OY 663 FTSTRPRGLKTDVKDYHIDOYSNLVESLSDEYLDEKRELFILVKYAKQLHIERNM 718   :	C;Keywords: delta-endotoxin Query Match Best Local Similarity 43.8%; Score 1480.5; DB 1; Length 1157; Best Local Similarity 43.8%; Pred. No. 4.1e-94; Matches 320; Conservative 117; Mismatches 229; Indels 65; Gaps 14;
cillus thuringiensis (str	QY 26 LKNETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTLGVPF 78   :::       :      :
-1992 #text_change 09-Jul-2004 any, C.S.; Johnson, T.B.; Gawron-Burke,	Qy 79 AGQVASLYSFILGELWPKGKNQ-WEIFMEHVEBIINQKISTYARNKALTDLKGLGDALAV 137
A.Title: Isolation and characterization of a novel insecticidal crystal protein gene from A.Reference number: A42459; MUID:91286178; PMID:2061280 A.Accession: B42459 A.Status: preliminary	Qy 138 YHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHL .197
A,Molecule type: DNA A,Residues 1-380 cCHA> A,Cross-references: UNIRROT:QBKY61; UNIPROT:Q45740; GB:M63897 C;Superfamily: parasporal crystal protein	Qy 198 LLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKNYSTGLNNLRGTNAESWVRY 257
Query Match Best Local Similarity 95.3%; Pred. No. 2.7e-123; Matches 362; Conservative 8; Mismatches 10; Indels 0; Gaps 0;	Cy 258 NOFREDWILMVLDLVALFPSYDTQMYPIKITAQLTREVYTDAIGTVHPHPSFISITWYNN 317
Qy 1 MKLKWQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 60	Cy 318 NAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWŠ-NTQYMNWWGGHKLEFRIG-GTLN 375 
QY 61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA 120	QY 376 ISTQGSTNTSINPUTLPFTSRDVRKTESLAGLNLFLTQPVNVPRVDFHWKFVTHPIA 432  1
QY 121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 	Qy 433 SDNFYYPGYAGIGTQLQDSENELPP-EATGQPNYESYSRRLSHIGLIS 479   1
QY 181 EEVPLLPIYAQAANLHLLILRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240	Qy 480ASHVKALVYSWTHRSADRINTIEFNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 533
Qy 241 TGLNNLRGTNAESWVRYNQFRRDWTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300 	QY 534 ILRRINIGIFGDIRVNINPPFAQRYRVRIRYASITDLQFHTSINGKAINQGNFSATWNRG 593
OY 301 GTVHPHPSFTSTTWYNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNWW 360 	Qy 594 EDLDYKTEXTVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYE 647 ::
Qy 361 GGHKLBFRTIGGTLNISTQG 380    :	Qy 648 AEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVK 707
, RESULT 7	Oy 708 YAKQLHIERNM 718

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Darasporal crystal protein crylFa3 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Dacesion: 832649
R;Lambert, B.
R;Lambert, B.
A;Reference number: 832645
A,Rccession: 832649
A;Reference number: 832645
A,Rccession: 832649
A;Status: preliminary
A,Rolecule type: DNA
A;Residues: 1-1174 < LAM
A;Residues: 1-1174 < LAM
C;Superferences: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g295865; Keywords: delta-endotoxin
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GNLESGNPRIAGFSTPFSFSNAQSTFTLGTQAFSN-QEVYIDRIEFVPAEVTFEAESDLE
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C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accession: 832645
R.Lambert, B.
Submitted to the EMBL Data Library, April 1993
A.Reference number: 832645
A.Accession: 832645
A.Accession: 832645
A.Accession: S32645
A.Accession: Sazes
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C.Species: 1-1166
C.Superiamily: parasporal crystal protein
C.Superfamily: parasporal crystal protein
C.Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLDFLEQVTIYSLLSRWSNTQYMNMWGGHKLEFRTIG-GTLN-----ISTQGSTNTS 385
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                                                                                                                                                                                                                                                                                                                                                                              Conservative 101; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                             Score 1462; DB 2;
Pred. No. 7.9e-93;
                                                                                                                                                                                                                                                                                                                                             39.0%;
AAKRLSRERNL
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Best Local Similarity
Matches 322; Conserv
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A,Molecule type: mRNA
A,Residues: 1-1155 <KON>
A,Cross-references: UNIPROT:P06578
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A, Status: preliminary
A, Molecule type: DNA
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Gene: cry-1-2; bt2
                                                                                                                            A; Accession: A90025
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paragoral crystal protein - Bacillus thuringiensis (strain aizawai)
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Datilus thuringiensis
C;Accession: A26513
R;Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
R;Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
A;Title: Nuclectide sequence of the insecticidal protein gene of Bacillus thuringiensis
A;Accession: A26513
C;Gyberians: 1-1155
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 NINHEDCLKMSEYENVE-PFVSASTIQTG----IGIAGKILGTLGVPFAGQVASLYS
                                                                                                                                                                                                                                                                                                                                                                                  4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLLSEF-VPGAGFVLGLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                       148 NRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 TOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNV-PRVDFHWKFVTHPIASDNF
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                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                 DB 2; Length 1155;
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                                                                                                                                                                                                                                                                                                    Best Local Sim
Matches 313;
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R;Gelser, M.; Schweitzer, S.; Grimm, C.
Rache 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal protes;
A;Reference number: A91560; MUID:87163505; PMID:3557124
A;Accession: A91560
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A; Residues: 1-1155 cCHA>
A; Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A; Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
B; Flotte, H, de Geree, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckl
Bur. J. Blochem. 161, 273-280; 1986
A; Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A; Reference number: A26461; MUID:87054026; PMID:3023091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene product analy
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parasporal crystal protein crylAb3 - Bacillus thuringiensis
NyAlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal (Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
A;XiKondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Axashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes is a paraspecies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;MOJecule type: DNA
A;Residues: 1-1155 <WAB>
A;Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720
A;Experimental source: subsp. berliner
R;Chak, K.F.; Jen, J.C.
submitted to the EMBL Data Library, October 1990
A;Description: Complete nucleotide sequence and expression in Escherichia coli A;Reference number: S14555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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A;Molecule type: DNA
A;Rossidues: 1-730,'L',732-784,'R',786-1155 <HOF>
A;Rossidues: 1-730,'L',732-784,'R',786-1155 <HOF>
A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A;Experimental source: strain berliner 1715
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
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A,Residues: 1-1155 <GEI>
A,Residues: 1-1155 <GEI>
A,CCOSS-TEGETENCES: GENES271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A,Experimental source: subsp. kurstaki
R,Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA S, 305-314, 1986
A,Title: Bacillus thuringiensis entomocidal protoxin gene sequence and grA,Reference number: A90955; MUID:86300092; PMID:3743328
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Best Local Similarity 44.2%; Pred. No. 2e-91;
Matches 314; Conservative 111; Mismatches 22
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'Keywords: delta-endotoxin

'82-586/Product: toxic peptide #status predicted

'82-300/Region: toxic #status predicted

'300-586/Region: insecticidal #status predicted
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148 NRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFG 207

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parasporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: A22798
R;Shibano, Y; Yamagata, A; Nakamura, N; Ilzuka, T; Sugisaki, H; Takanami, M.
C;Accession: A243-251, 1985
A;Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuring A;Reference number: A22798; MUID:85232070; PMID:2989108
A;Accession: A2279
A;Accession: A2279
A;Molecule type: DNA
A;Residues: 1-934 c&HI:
A;Cross-references: UNIPROT:Q985V8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
C;Comment: The authors translated the codon ACA for residue 264 as Ser.
C;Keywords: delta-endotoxin
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                                        GIEGS-IRSPHLMDILNSITIYTDAHRGEYYWSGHQIMASPVGFSGFEFTFPLYGTMGNA
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                                                                                     VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S
                                                                                                         324 AIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNTQYMMM---WGGHKLEFRTIGGTLNI
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                                                                                                                                                                                                                              STOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNV-PRVDFHWKFVTHPIASDN
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Best Local Si
Matches 308;
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A2012911 A2 - Bacillus thuringiensis subsp. Kurstaki (strain HD-1)
C;Decession: A29125
A20129
A;Hischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A;Hitle: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Accession: A29125
A;Accession: A29125
A;Accession: A29125
A;Accession: A29125
A;Accession: A29125
A;Coss-references with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Accession: A29125
A;Coss-references: UNIPROT;O97295; UNIPROT;O93721
C;Superfamily: parsaporal crystal protein
C;Keywords: delta-endotoxin
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DPINPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANIHLSVIRDVSVFG 179
                                                  KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNOFRRDMTLM 267
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                                                                                                                                            STOGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNV-PRVDFHWKFVTHPIASDN 435
                                                                                                                                                                                                                                                                                      345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTERAYG----TSSN 395
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38.5%; Score 1441.5; DB 2; Length
Best Local Similarity 44.2%; Pred. No. 2.1e-91;
Matches 314; Conservative 111; Mismatches 228; Indels
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A;Residues: 1-1176 <UDA>
A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g53578
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C;Species: Bacillus thuringiensis
C;Accessis Dacillus thuringiensis
C;Accession: UC2219
E;Adayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Osci. Biotechnol. Biochem. 58, 830-835, 1994
A;Title: Cloning of a new crylA(a) gene from Bacillus thuringiensis strain FU-2-7 and A;Reference number: JC2219; MUID:94289859; PMID:7764972
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CRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLT 239
                                                                                                                                                         449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQIS 508
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                                                       VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327
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                                                                                                                                 AV---VRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLEFRTIGGT---LNISTQGS
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38.0%; Score 1426; DB 2;
Best Local Similarity 43.0%; Pred. No. 2.5e-90;
Matches 307; Conservative 118; Mismatches 223;
                                                                               240 VLDIVALFSNYDSRRYPIRTVSQLTREIYTNPV---
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C,Superfamily: parasporal crystal protein
C,Keywords: delta-endotoxin
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A;Residues: 1-1176 <SHI>
A;Residues: 1-1176 <SHI>
A;Cross-references: UNIPROT:P02965
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protei
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATIONATE DATE OF THE PROCESS OF THE PROCESS (Strain algamas IPL7)

NATHCATHER DAMES: 135K Insecticidal protein

C,Species: Bacillus thuringiensis

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

R;Ancession: Johie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.

Agric: Biol. Chem. 52, 1565-1573, 1988

Arithe: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein

A;Accession: JT0241
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                                                             VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA
                                                                                                                                       328 AV----VRNPHILDFLEQVTIYSLLSRWSNTQYMNMWGGHKLEFRTIGGT----LNISTQGS
                                                                                                                                                             382 INTSINPVILPFISRDVYRIESL------AGLN---LFLIQPVNVPRVDFHWKFVTH
                                                                                                                                                                                                                                                                                         430 PIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS----HVK
                                                                                                                                                                                                                                                                                                                           396 NLPSTIYRQRGTV-----DSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLR
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QRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLT		VLDIVALFSNYDSRRYPIRTVSQLTREIYTNPV	AVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNWWGGH	RIEQNIRQPHLMDILNSITIYIDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGN	TNTSINPVTLPFISRDVYRTESLAGLNLFLTQPVNVPRVDFHWKFVTH	AGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASUTT	PIASDNFYYPGYAGIGTQLQDSENELPPEATGOPNYESYSHRLSHI		ALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGTFG	APTESWQHRSAEFNNIIPSSQITQIPLIKSTNLGSGTSVVKGPGFTGGDILRRTSPGQIS	DIRVNINDPFAQRYRVRIRYASTIDLQFHISINGKAINQGNFSATWNRGEDLDYKTFXTV	TRAVNITAPLSQRYRVRIRYASTINLQFHISIDGRPINGGNFSATMSSGSNLQSGSFRIV	GFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAAEYDFEKAQEKVTALFT	GETTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFT	SINPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFELVKYAKQLHIERNM	SSNQIGLKTDVTDYHIDQVSNLVECLSDEFCLDEKQELSEKVKHAK	
180	268	240	328	286	382	341	430	396	485	449	545	509	605	569	665	629	
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Search completed: October 28, 2004, 18:31:47 Job time: 21.1643 secs

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October 28, 2004, 18:10:58 ; Search time 65.5881 Seconds (without alignments) 3549.224 Million cell updates/sec
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3749
1 MKLKNQDKHQSFSSNAKVDK.......KRELFEIVKYAKQLHIERNM 718
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| cgn2_6/ptodata/2/pubpaa/VSC7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT7_REW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSC6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSC6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSC6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NSC8_NEW_PUB.pep:*
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
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			Description	Sequence 10, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 7, Appli	4.2	Sequence 10, Appl	Sequence 7, Appli	~	Sequence 23, Appl		•	•	Sequence 1, Appli
SUMMARIES			סד	US-10-782-020-10	US-10-782-141-8	US-10-782-096-10	US-10-782-570-7	US-10-428-961-42	US-10-809-953-10	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23	US-10-428-961-38	US-10-614-524-2	US-09-826-660-25	US-10-089-678-1
			ВВ	17	17	17	17	14	16	10	14	σ	14	15	σ	14
			Match Length DB I	719	719	719	719	710	1228	1207	1227	1186	1228	1228	643	1167
	960	Query	Match	99.3	99.3	99.3	99.3	91.7	0.09	59.6	57.5	57.1	55.6	55.6	50.7	45.6
			Score	3722.5	3722.5	3722.5	3722.5	3439	2249	2236	2156	2141	2085.5	2085.5	1902	1708
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Sequence 6, Appli Sequence 17, Appl Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 17, Appli Sequence 17, Appli Sequence 11, Appli	Sequence 28, Appl Sequence 4, Appli Sequence 10, Appli Sequence 12, Appli Sequence 2, Appli Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli
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## ALIGNMENTS

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                                      RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
                                                                                                                                                                  TGLNNIRGTNAESWVRYNQFRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREVYTDAI 300
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                                                                                                                 181 BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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                                                                                 EEVPLLP1YAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                                                                                                         Score 3722.5; DB 17; Length 719;
Pred. No. 1.7e-302;
0; Mismatches 3; Indels 1;
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Publication No. US20040197917A1

GENERAL INFORMATION

APPLICANT: Garzii, Nadine

APPLICANT: Hargiss, Tracy

APPLICANT: Koziel, Micholas B.

APPLICANT: Carr, Brian

CINERNT: Carr, Brian

FILE REFERENCE: 045600/274143

CURRENT FILING DATE: 2004-02-20

PRIOR APPLICATION NUMBER: 60/448,632

PRIOR FILING DATE: 2003-02-20

NUMBER: CARRENT SOURCES CONTINUMBER: CARRENT SOURCES CONTI
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Best Local Similarity 99.4%;
Matches 715; Conservative
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LENGTH: 719
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1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                              EEVPLLPIYAQAANIHILLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
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                                              OTGIGIAGKILGTLGVPFAGOVASLYSFILGBLWPKGKNOWEIFMEHVEELINQKISTYA
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publication No. US20040210964A1

GENERAL INPORMATION:
APPLICANT: Carczi, Nadine
APPLICANT: Rargiss, Tracy
APPLICANT: Roziel, Micholas B.
APPLICANT: Carc, Brian
ITILE OF INVENTION: Actholas B.
ITILE OF INVENTION: Mcthods for Its Use
TILE REPERBNCE: 045600/274148
CURRENT APPLICATION UNMBER: US/10/782,096
CURRENT FILING DATE: 2004-02-19
PRIOR PILIOR DATE: 2004-02-19
PRIOR PILIOR DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 7, Application US/10782570

Publication No. US20040210965A1

GENERAL INFORMATION:
APPLICANT: Acarozzi, Nadine
APPLICANT: Acarozzi, Nadine
APPLICANT: Acarozzi, Michael G.
APPLICANT: Carr. Brian
ITILE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
ITILE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
ITILE OF INVENTION: Methods for Its Use
FILE REPERENCE: 0456.00/274144

CURRENT FILING DATE: 2004-02-19

PRIOR APPLICATION NUMBER: 60/448,812

PRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 719
                Indels
 Pred. No. 1.7e-302;
0; Mismatches 3;
  99.48;
 al Similarity 99.4
715; Conservative
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Sequence 42, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
APPLICANT: Buum, James A.
APPLICANT: Chu, Chih.Rei
APPLICANT: Chu, Chih.Rei
APPLICANT: Bumer, Amy J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201-1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
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                                                                                                                                                                       1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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                                                                                     719;
                                                                                                                              1,
                                                                                   Score 3722.5; DB 17; Lengt
Pred. No. 1.7e-302;
0; Mismatches 3; Indels
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7
                                                                                 99.3%;
al Similarity 99.4%;
715; Conservative
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US-10-428-961-42
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         APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESS
TITLE OF INVENTION: CRYSTAL PROTEINS
FILE REFERENCE: 021565-078
CURRENT APPLICATION NUMBER: US/09/661,016
PRIOR APPLICATION NUMBER: PCT/EP90/00905
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 1990-05-30
PRIOR FILING DATE: 1990-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver: 2.0
SOFTWARE: PatentIn Ver: 2.0
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Bacillus thuringiensis
US-10-809-953-10
Van Mellaert, Herman
Botterman, Johan
Van Rie, Jeroen
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NAME/KEY: misc feature
LOCATION: (2007)...(2000)

LOCATION: (2007)...(2000)

US-10-428-961-42
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                                                                                                                                                                                                                 Length 710;
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PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION WUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 42
LENGTH: 710
                                                                                                   TYPE: PRT ORGANISM: Bacillus thuringiensis
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RESULT 6
US-10-809-953-10
is equence 10, Application US/10809953
i Publication No. US20040181825A1
i GENERAL INFORMATION:

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249

367

451

603

691 663

Gaps

14;

Length 1227; Indels

631

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APPLICANT: Baum, James A.
APPLICANT: Chu, Chin.Rei
APPLICANT: Donovan, William P.
APPLICANT: Ornovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
TILLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TILLE OF INVENTION: Polymucleotides, Compositions, and Methods of Use (Amended)
FILE REPREMENTE: Lepidopterant US/10/428,961
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
NUMBER OF SEQ ID NOS: 63
SOPTWARE: PatentIn Version 3.2
                                                                                                                                                                                                                                                                            EQUTIVELLSRWSNTQYMNWGGHKLEPRTIGGTLNISTQGSTNTSINPVTLPFTSRDVY 399
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                                                   572 FHTSINGKAINQGNFSATMNRGEDLDYKTFXTVGFTTPFSLLDVQSTFTIGAWNFSSGNE
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                                                                                                                                                                                             TQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFL
                                                                                                                                                                                                                                                                                                                                                                RIESLAGINLF--LIQPVN-VPRVDFHWKFVTHP----IASDNFYYPGYAGIGTQLQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 VKAFNLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDLO
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ilarity 58.8%; Pred. No. 6.1e-171;
Conservative 105; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFYLDEKRELFEIVKYAKQLHIERNM 718
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, Sequence 63, Application US/10428961
, Publication No. US20030237111A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Bacillus thuringiensis
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Matches 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 EDCLKMSEYENVEPFVSASTIQTGIGLAGKILGTLGVPFAGQVASLYSFILGELWPKGKN
656 FININPRRLKIDVIDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
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                                                                                                                                                                                                                                                                                                                                                                              SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1207;
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/98,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION: <u >CUNKNOWN></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.6%; Score 2236; DB 10;
63.9%; Pred. No. 1.2e-177;
iive 78; Mismatches 156;
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APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 8-188051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Syngenta Biotechnology,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                          Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                           US-09-988-462-7

Sequence 7, Application US/09988462

Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Lewis, Rally S.

Kramer, Vance C.

Marren, Gregory W.
                                                                                                                                                                                                                                                                     Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919)541-8689
N FOR SEC ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9. CORRESPONDENCE ADDRESS
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Matches 439, Conservative
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                                                    IAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKAL 125
                                                                                                                           122 ARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQBVPL 181
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SSNAKVDKISTDSLKW-----ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIG 65
                          61
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Patent No. US20010026940A1

GENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Or UNENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1

CURRENT FILING DATE: 1998-10-23

PRIOR PILING DATE: 1998-10-23

PRIOR PELING DATE: 1998-10-23

PRIOR PLING DATE: 1998-11-12

PRIOR PLING DATE: 1998-03-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING DATE: 1998-03-02

SOFTWARE: PATENTING DATE: 1998-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANBSLTSQSFRFA
              186 LPIYAQAANLHLILLERDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNN
                                                                                                                                                                                 EFRIIGGTLNISTOGSTNISINPVILPFISRDVYRTESLAGLNLFLIOPVN-VPRVDFHW
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ORGANISM: Artificial Sequence
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LENGTH: 1186
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US-09-826-660-23
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Sequence 38, Application US/10428961
Sequence 38, Application US/10428961
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Rupar, Mark J.
APPLICAN
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                                                                                                                                                                                               13 SSNAKVDKISTDSLKN-----ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIG
                                                                                                                                                                                                                                   62 IAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEQLIRQQVTENTRDTAL
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                                                                                                                                                   Gaps
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                                                                                           Length 1186;
                                                                                              Query Match
57.1%; Score 2141; DB 9; Length 1
Best Local Similarity 58.5%; Pred. No. 1e-169;
Matches. 418; Conservative 108; Mismatches 174; Indels
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t.
US-09-826-660-23
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US-10-428-961-38
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|GDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186
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                                                                                                                                                                                                                                                                                          DB 14; Length 1228
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PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 38
                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38
                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 421; Conservative
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US-10-614-524-2
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                                  from Bacillus thuringiensis
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59.0%; Pred. No. 4.9e-165;
ive 98; Mismatches 183; Indels
APPLICANT: Van Rie, Jeroen
TITLE OF INVENTION: Insecticidal proteins fro
FILE REFERENCE: NEWBETSUS;
CURRENT APPLICATION NUMBER: US/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Bacillus thuringiensis
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RESULT 12 US-09-826-660-25

Sequence 2, Application US/10614524
Publication No. US20040016020A1
PERENEAL INFORMATION:
APPLICANT: Arnaut, Greta
APPLICANT: Boete, Annemie
APPLICANT: Damme, Nicole
APPLICANT: Mathieu, Eva

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Sequence 1, Application US/10089678 Publication No. US20030017967A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    Bacillus thuringiensis
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANITATION
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                                     US-10-089-678-1
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                                  APPLICANT: Gardineau, Guy A.
APPLICANT: Gardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: Ma-74AC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR PELLOR NUMBER: 60/065,215
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR APPLICATION NUMBER: 60/065,445
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 643
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                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene US-09-826-660-25
                                                                                                                                                                                                                                                                                                                                        50.7%; Score 1902; DB 9;
57.2%; Pred. No. 4.2e-150;
tive 100; Mismatches 161;
Sequence 25, Application US/09826660 Patent No. US20010026940A1
                                                                                                                                                                                                                                                                                                                                                                    Conservative 100;
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                        Similarity
                Patent No. US20010020
GENERAL INFORMATION:
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Best Local Simi
Matches 368;
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APPLICANT AGANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REFERENCE: 068821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: PT/JP01/06660
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2010-08-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 11-07
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Best Local Similarity 47.4%; Pred. No. 1.9e-133;
Matches 357; Conservative 126; Mismatches 222;
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529
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                                                                      537 -RINTGTF---GDIRVNIN-PPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMN 591
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1 MSPNNQNEYEIIDATPST-SVSSDSNRYPFANEPTDALQNMNYKDYLKMSGGENPELFGN
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                                                                                                    530 INRNNGNIQNRGYIEVPIQFTSTRYRVRVRYASVTSIELNVNLGNSSIFTNTLPATAA
                                                                                                                                                          592 RGEDLDYKTFXTVGFTTPFSLLDVQSTFT-----IGAWNFSSGNEVYIDRIEFVPVEVT
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PUblication No. US20040197917A1
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargiss, Track
APPLICANT: Buck, Nichael G.
APPLICANT: Cariel, Michael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: ARMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for its Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.1%; Score 1652; DB 17;
48.8%; Pred. No. 9e-129;
ive 100; Mismatches 229;
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FILE REFERENCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 6/448,632
PRIOR APPLICATION NUMBER: 6/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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TYPE: PRT
ORGANISM: Bacillus thuringiensis
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641 FEVEYDLERAQK 652
                                                                                                                                                                                                                                              646 YEAEYDFEKAQE 657
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Best Local Si
Matches 369;
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Sequence 6, Application US/10428961

Subjection No. US20030237111A1

SERNERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Baum, William P.
APPLICANT: Chu, Chih.Rei
ITIER OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
ITIER OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
ITIER OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
ITIER OF INVENTION: Rolymcleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201-1

CURRENT RAPLICATION NUMBER: 09/661,322
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 1999-09-15
SPRIOR PILING DATE: 1999-09-15
SPRIOR PILING DATE: 1999-09-15
SPRIOR PILING DATE: 1990-09-15
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                         70 ILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKALTDLK 129
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44.2%; Score 1658; DB 14;
Best Local Similarity 51.3%; Pred. No. 1.2e-129;
Matches 345; Conservative 104; Mismatches 175;
                                                                                                             LVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
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Search completed: October 28, 2004, 18:40:53 Job time : 68.5881 secs

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MOLECULE TYPE: protein
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-261-322A-42
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US-09-203-2170A-4
US-09-218-942-2
US-08-100-709-4
US-08-11-340-4
US-08-17-9-046-4
US-08-17-9-046-4
US-08-17-9-046-4
US-08-17-9-046-4
US-08-17-9-046-4
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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29 2005 5 5 6 1228 4 18-09-18-28-39 Sequence 25, Appl 201 1902 50.7 643 4 105-09-18-28-35 Sequence 25, Appl 201 1902 50.7 643 4 105-09-18-28-55-6 Sequence 25, Appl 201 1902 50.7 643 4 105-09-18-28-6-5 Sequence 25, Appl 201 1903 50.4 41.2 1537 105-09-10-28-6-6 Sequence 25, Appl 201 1903 50.4 41.2 1537 105-09-10-28-6-13-28-6 Sequence 25, Appl 201 1903 50.4 41.2 1537 105-09-10-28-6-13-28-6 Sequence 27, Appl 201 1903 50.4 41.2 1537 105-09-10-28-6-13-28-6 Sequence 27, Appl 201 1903 50.4 41.2 1537 108-09-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-6-19-28-
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Gaps

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TGTFQDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQCNFSATWARGEDLDYK 599
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                                                                                                                                                                                                                                             BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
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                                                                                                                                                                 1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
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                                                                                                         Length 710;
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                                                                                                      Query Match 91.7%; Score 3439; DB 4; Best Local Similarity 91.9%; Pred. No. 1.1e-299; Matches 661; Conservative 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                NAME/KEY: misc_feature
LOCATION: (200)
CTHEN INFORMATION: No. 6593293-Coding
US-09-661-322A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-286-870A-4; Sequence 4, Application US/08286870A; Patent No. 6063605
Bacillus thuringiensis
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APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Glimer, Amy J.
APPLICANT: Glimer, Amy J.
APPLICANT: Glimer, Amy J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT APPLICATION NUMBER: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
SEQ ID NO 42
LENGTH: 710
TYPE: PRT
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                                                                                        1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
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                                    Gaps
                                                                1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                    ä
    Length
                                    Indels
      DB 3;
                                   3;
    99.2%; Score 3718.5;
llarity 99.3%; Pred. No. 0;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 42, Application US/09661322A; Patent No. 6593293; GENERAL INFORMATION:
                      Similarity
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US-09-661-322A-42
                        Local Sim
es 714;
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541 IGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600 TEXIVGETIPESLLDVQSTFTIGAMNESSGNEVYIDRIEFVPVEVTYE 647 601 TPRIVGFITPFSFLDVQSTFTIGAWNPSSGNEVYIDRIEFVPVEVTYE 648 RESULT 4 US-09-003-217-2 540 d ò g ð COMPUTER ERADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1980
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. XCKULIS
REGISTRATION NUMBER: 16,773
REGISTRATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LUNGWATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LUNGWATION FOR SEQ 1D NO: 4:
LUNGWATH: 6,48 main a caids
LUNGTH: 6,48 main a caids ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. : 648 amino acids amino acid TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein CIT:
SIATE: DC
COUNTRY: USA
TT: 20005-3918

540 539

18-10-013-823D-34.ra1

OCC 47 TO:OO:43

QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA 120 181 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240 61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA 120 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 BEVPLLPIYAQAANLHILLIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240 TGLNNLRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300 241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW 360 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNIFLTQPVNGVPR 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 479 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 60 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI Gaps , , Score 3360.5; DB 3; Length 648; Pred. No. 1e-292; 0; Mismatches 3; Indels 1; 89.6%; Query Match Best Local Similarity 99.49 Matches 644, Conservative 241 61 181 301 301 361 120 121 qq Dp ð 음 g à 엄 à 엄 g ò 8 ∂ à

EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSBISTFYNRQVERAGDYSYHCVKWYS 240

181

61 OTGIGIAGKILGTLGVEPPPGQIASLYSFILGELWPKGKSQWEIFWEHVEAIINRKISTYA 120 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 9 9 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA 1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 1 MKLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI Gaps 1; Length 719; Sequence 2, Application US/09003217; Patent No. 598617; Patent No. 598617; GENERAL INFORMATION:
APPLICANT: Osman, Yehia A. APPLICANT: Madkour, Magdy A. APPLICANT: Bulla, Lee A. APPLICANT: Balla, Lee A. CORRESSER: W. Murray Spruill (Alston & Bird, LLP) STREET: 3605 Glenwood Ave. Suite 310
STREET: 3605 Glenwood Ave. Suite 310
STATE: NC
COUNTRY: US
ZIP: 27622 Query Match 89.6%; Score 3358.5; DB 2; Length Best Local Similarity 89.6%; Pred. No. 1.9e-292; Matches 644; Conservative 33; Mismatches 41; Indels COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE: CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REPRENCE/DOCKET NUMBER: 5718.
TELEPHONE: 919 420 2202
TELEFAX: 919 481 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS: LENGIH: 719 amino acids , MOLECULE TYPE: protein US-09-003-217-2 amino acid TOPOLOGY: 61 8 임 ଟ В ò

US-08-286-870A-4

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           EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240
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                                           BEVPLLPIYAQAANLHLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWNN
                                                                                                      GGHRLESRPIGGALNTSTYGGSTNTSINPVTLQFTSRDFYRTESWAGLNLFLTQPVIGVPR
                                                                                TGLNNLRGINAESWVRXNQFRRDMILMVLDLVALFPSYDTOMYPIXTTAQLTREVYTDAI
                                                                                                                                                           GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
                                                                                                                                                                                                                                                                                                           VDPHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                  GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPV-NVPR
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MEDIUM TYPE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFTAMION A35
PRIOR APPLICATION A35
FILING DATE: 09-WAY-1990
PRIOR APPLICATION NUMBER: US 07/520228
FILING DATE: 09-WAY-1990
PRIOR APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-WAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Intellectual Property Group of SSEE: PILLSBURY, MADISON & SUTRO LLP I: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ELY, S.
APPLICANT: TALOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
TUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08286870A Patent No. 6063605 GENERAL INFORMATION:
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ADDRESSEE:
STREET: 110
CITY: Washi:
STATE: DC
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
TITLE OF INVENTION: Activity
FILE REFERENCE: CTY1
CURRENT APPLICATION NUMBER: US/09/218,942
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/035,361
EARLIER PILING DATE: 1997-01-10
EARLIER PILING DATE: 1998-01-06
NUMBER: OS EQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                                                                                                                            EEVPLLPIYAQAANLHLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWNN
                                                                                                            GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
                                                                                                                                                                                 GCHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
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                                     TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                       1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIBLQNINHEDCLKMSEYBNVEPFVSASTI
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89.5%; Score 3356.5; DB 3; Length 719;
Best Local Similarity 89.6%; Pred. No. 2.8e-292;
Matches 644; Conservative 33; Mismatches 41; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/09218942; Patent No. 6232439; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Bacillus thuringiensis
US-09-218-942-2
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US-09-218-942-2
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18-10-019-873D-01-81

NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHOME: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6; SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acid
TYPE: amino acid / MOLECULE TYPE: protein US-08-286-870A-6

Gaps 1; Length 535; 1; Indels Score 2778.5; DB 3; Pred. No. 1.4e-240; 0; Mismatches 1; I 74.18; 99.68; Query Match
Best Local Similarity 99.6
Matches 533; Conservative

9 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI

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RNKALIDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 121

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ASHVXALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 481

535

Sequence 4, Application US/08100709 Patent No. 5322687 GENERAL INFORMATION:

APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: PACILLUS THURINGIENSIS cryer4 AND cryer5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
TITLE OF INVENTION: ADDRESS:
ADDRESSE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia

COUNTRY: U.S.A.

ZIP: 19103
COMPITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARDICATION BATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSITICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EGOLF, Christopher: ATTORNEY/AGENT NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
L'ENGTH: 1229 amino acids TOPOLOGY: linear MOLECULE TYPE: protein

18; Length 1229; 64.4%; Score 2415; DB 1; Length 1 65.1%; Pred. No. 2.3e-207; ive 91; Mismatches 141; Indels Query Match Best Local Similarity 65.1<sup>§</sup> Matches 467; Conservative

99 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEVNNIDPFVSASTVQTGINIAGRI 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGLAGKI

130 67 LGVLGVPFAGQLASFYSFLVGELMPSGRDPWEIFLEHVEQLIRQQVTENTRNTAIARLEG 126 LGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186 LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYARNKALTDLKG LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYA 71 à g ð 임

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AESWVRXNQFRRDMTLMVLDLVALFBSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310 247 AESWLRYNOPRRDLILGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRINAPSGFA 306 251 d ò g

STTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNWWGGHKLEFRTI 370 311

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481 GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPRVDFHWKFVT 367 GGILNISIQGLINNISINPVILQFISRDVYRTESNAGINILFTIPVNGVPWARFNF----429 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS 371

423 --INPONIYERGATTYSOPYOGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLIIGN 482 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 541 TFGDIRLNINVPLSQRYRVRIRYASTTDLQFFTRINGTTVNIGNFSRTMNRGDNLEYRSF TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 542 g ò

602 XTVGFTTPFSLLDVQSTFTLGAWNFSSGNBVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA

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540 601

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APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Ganzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CIVET4 AND CIVETS
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            247 AESWLRYNQFRRDLILGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRINAPSGFA 306
                                                                                                                                                                                                                                                 662 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
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                                                                                                                                            GGTLNISTOGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPRVDFHWKFVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/100,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: EGOLf, Christopher
REGISTRATION NUMBER: 27633
REFERENCS/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jose M.
TITLE OF INVENTION: DAIL GENERAL THORINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
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                             662 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
                                                       QAANLHLLLLLRDASI FGKEWGLSSSEI STFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN
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65.1%; Pred. No. 2.38-207;
ive 91; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLF, Christopher:
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-757-159
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  ; Sequence 4, Application US/08176865; Patent No. 5616319; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: 1:---
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Best Local Similarity 65.1%
Matches 467; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Panitch Schwarze Jacobs & Nadel
ADDRESSEE: Panitch Schwarze Jacobs & Ne ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania STATE: Pennsylvania ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 43.5
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: 8901f, Christopher
REGISTRATION NUMBER: 72633
REFERENCE/DOCKET NUMBER: 7205-49
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
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Best Local Similarity 65.1%
Matches 467; Conservative
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3Y: linear
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APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Ganzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                          18;
                                                                                                                                                                          Length 1229;
                                                                                                                                                                        64.4%; Score 2415; DB 1; Length 12
65.1%; Pred. No. 2.3e-207;
ive 91; Mismatches 141; Indels
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Sequence 4, Application US/08779046
Patent No. 5854053
GENERAL INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                  Query Match
Best Local Similarity 65.1%;
Matches 467; Conservative
                                                                                           ; MOLECULE TYPE: protein US-08-474-038-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STIWYNNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNIQYMNMWGGHKLEFRII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 SSNAKVDKISTDSLKN-ETDIBLQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGLAGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN
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65.1%; Pred. No. 2.38-207;
ive 91; Mismatches 141; Indels
A.S.
                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
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99

190

250 246 428 422

366

422

541 540 601 600 661

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RESULT 12
US-08448-170-10
US-08448-170-10
Sequence 10, Application US/08448170
Sequence 10, Application US/08448170
September 10, Application US/08448170
SENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth B.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. F8158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
                                                                                                                                                                                                                 --INPONIYERGATTYSOPYOGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLIIGN 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 LGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186
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                                                                                               481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRINTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 TFGDIRVNINPPFAQRYRVRIRYASTIDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
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                                                                                                                                                                                                                                                                                                   STIWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMGGHKLEFRTI
                                                                                                                                                                                                                                                                                                                                         STWENNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYWVGHRLNFRPI
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448.170
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424
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CLASSIFICATION:
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COUNTRY: USA
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Patent No. 5942658
GENERAL INPORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACTLLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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                                                                                                                              661
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                                                                                                                                                                                                                                                 662 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
                                                                                                                                                                                                                                                                                       LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNL 716
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         TEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
                                                                                                                           602 XTVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA
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65.1%; Pred. No. 2.3e-207;
cive 91; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-UW1-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1601 Market Street, 36th Floor
Philadelphia
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APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORWATION:
NAME: ESPEL, CALLSTACHORS
RECISTRATION NUMBER: 27633
REFRENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-159
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
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LENGTH: 1229 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pennsylvania
: U.S.A.
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US-08-881-340-4
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                                                                                                                                                                                                                                                                                                             099
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               542
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Best Local (
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RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 488;
       Encoding Lepidopteran-Active Toxins
                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%; Score 2319; DB 3;
89.3%; Pred. No. 2.1e-199;
ive 13; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: M/S 102DCD1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 10:
                                               SSEE: Jay M. Sanders
1: 2421 N.W. 41st Street, Suite
Gainesville
                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-UNE-1993
CLASSIFICATION: 000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAX-1995
CLASSIFICATION: 000
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
                                                                                                                                                                                         i: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 amino acids
amino acid
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Matches 444; Conservative
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LENGTH: 488 amino aci
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                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                   ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                               OPERATING SYSTEM:
     INVENTION:
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                                                                                                                   Florida
: USA
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                                                             ADDRESSEE:
                                                                                             CITY: Gai
STATE: F1
COUNTRY:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 102D.CT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                   INFORMATION: (904) 375-8100
TELERAX: (904) 372-8000
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTER.STICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS
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352 GGHKLEFRTIGGTLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTGPVNGVPR 411
                                                                                           GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
                                                                       VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-5EP-1992
CLASSIFICATION NUMBER: US/07/951,715A
FILING DATE: 45-5EP-1992
CLASSIFICATION UNDARE: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           Sequence 7, Application US/07951715A Patent No. 5625136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rothstein, Steven J.
Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                              Moziel, Michael G. Desai, Nalini M. Lewis, Kelly B. Kramer, Vance C. Warren, Gregory W. Crossland, Lyle D. Vright, Martha S. Merlin, Ellis J. Launis, Karen L.
                                                                                                                                                                          ASHVKALVYSWTHRSAD 488
                                                                                                                                              480 ASHVKALVYSWTHRSAD 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suttie, Janet L. TITLE OF INVENTION: SYNTHET TITLE OF INVENTION: INSECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
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CITY: Hawthorne
STATE: New York
COUNTRY: USA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-07-951-715A-7
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US-07-951-715A-7
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Score 2236;

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Query Match

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                                                                                                       TOMYPIKTTAQLIREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFL 339
                                                                                                                                                                                                                                                             ENELPPEATGOPNYESYSHRISHIGLISASHVKALVYSWTHRSADRTNTIEPNSITOIPL 511
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                                                                                                                                         160 SQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLLRDASIFGKEWGLSSSEIST 219
                                                                                                                                                                                                                                                                                                                                                     451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHISINGKAINQGNESAIMNRGEDLDYKIFXIVGFIIPFSLLDVQSIFTIGAMNFSSGNE 631
                                                   10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRD 69
                                    EDCLKMSBYENVEPFVSASTIQTGIGIAGKILGTLGVPFAGOVASLYSFILGELWPKGKN
                                                                                                                                                                                             FYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYD
                                                                                                                                                                                                                                                                                                                                                   RTESLAGINLF--LTQPVN-VPRVDFHWKFVTHP----IASDNFYYPGYAGIGTQLQDS
            Gaps
           14;
            Indels
ed. No. 2.6e-191;
Mismatches 156;
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 Pred. No.
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Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Best Local Similarity 63.9%; Pr.
Matches 439; Conservative 78;
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Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
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Suttie, Janet
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APPLICANT: Koziel
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US-08-459-448A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDVY 367
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   SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE 94
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENITITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE CORRESPONDENCE: 94
CORRESPONDENCE ADDRESS: ADDRESSE: No. 5853336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: US/-UN-1995
CLASSIFICATION DATA:
APPLICATION DATA: US/-UN-1995
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA: DATA: APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PACE, GATY M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUTCATION INFORMATION:
TELEPHONE: AT 1852
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TOPOLOGY: 1:1207
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 63.9°
Matches 439, Conservative
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MEDIUM TYPE: Floppy
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452 ENELPPEATGOPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 511
                                            424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQIPM
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                                                                                                                        512 VKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQ
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(c) 1993 - 2004 Compugen Ltd.
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PO6578 bacillus th Q7be98 bacillus th Q9£296 bacillus th	94 bacillus 02 bacillus bacillus bacillus	Weelx3 Dacillus th Q93t21 Dacillus th Q6pyw7 Dacillus th Aas93798 Dacillus	Q9s5v8 bacillus th Q7wzt9 bacillus th Q03748 bacillus th
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## ALIGNMENTS

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AC 045752 POTO (Rel. 39, Created)

AC 045752 POTO (Rel. 39, Created)

BY 04772 POTO (Rel. 39, Created)

CONTROL ON (Rel. 39, Created)

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601 TFRIVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
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EMBL; AZC2167; AAP86782.11 -.
ENTERPY: IPROUS638; endotoxin_C.
InterPro; IPROUS639; endotoxin_N.
InterPro; IPROUS639; endotoxin_N.
InterPro; IPROUS639; endotoxin_N.
InterPro; IPROUS639; endotoxin_N.
InterPro; IPROUS55; Endotoxin_C; 1.
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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100.0%; Pred. No. 2.6e-253;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Matches 719; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              Selvapandiyan A., Bhatnagar R.K.;
"Isolation, cloning and expression of cryV gene.";
"usolation, cloning and expression of cryV gene.";
submitted (C-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- polithelial cells of certain coleopteran and lepidopteran species.
Active on Plutella xylostella and Benbyx mori.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
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D -> Y (in strain JHCC4835 and strain HD-
1).
A -> V (in strain AB88).
KQ -> NE (in strain HD-1 and strain 61).
3627E5A6C25DAFF5 CRC64;
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MISCELLANEOUS: Toxic segment of the protein is located in the
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Best Local Similarity, 100.0%; Pred. No. 2.6e-253;
Matches 719; Conservative.....0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal bind like.
Pfam; PP03944; Endotoxin.N.; IPGam; PP03945; Endotoxin.M.; IPGam; PP03945; Endotoxin.M.; IPGam; PP03945; Endotoxin.N.; IPGam; PP03945; IPGam; PP0394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 443 A
711 712 KC
719 AA; 81216 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M98544, AAA22354.1, --
EMBL, X62821; CAA44633.1; --
EMBL, L36338, AAC3699.1, --
EMBL, L9391; AAC80058.1; --
EMBL, Y08920; CAA70124.1; --
PIR, 139815, 133815.
PIR, S25383, 53583.
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VARIANT 19
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                                                                                                                                                                                                                                                                                     VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                                                                                                                         ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                                                                                                                                                                                                    ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
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TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                      TGLNNLRGTNAESHVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                    GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
                                                                                                                                                                     GGHKLBFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                       VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SONG F., Zhang J., Gu A., Huang D., Li G.;

Submitted (APR-2010) to the EMBL/GenBank/DDBJ databases.

EMBL, AF373207, AAK66742.1; -.

R HSSP, PO2565, 10TF.

GO, GO.00055102; F:receptor binding; IEA.

GO, GO.0005405; P:pathogenesis; IEA.

R GO, GO.000405; P:pathogenesis; IEA.

InterPro; IPR001178; Endotoxin.C.

InterPro; IPR005539; endotoxin.N.

InterPro; IPR005539; endotoxin.N.

FEAM; PF03944; Endotoxin.C; 1.

R FEAM; PF03955; Endotoxin.M; 1.

R FEAM; PF03955; Endotoxin.N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
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99.9%; Pred. No. 5.8e-253;
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Bacteria, Firmicutes, Bacillales, Bacillaceae,
NCBI_TaxID=1428,
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01-DEC-2001 (TrEMBLrel. 19, Le
01-MAR-2004 (TrEMBLrel. 26, L.
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                    GTVHPHPSFTSTTWYNNNAPSFSA1EAAVVRNPHLLDFLEQVT1YSLLSRWSNTQYMNMW
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STRAIN-T01 328;
BEDINDOLO R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
Espindolota R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
"Complete sequence of cryll gene of isolate T01 328 from 1thuringiensis from Cubatao (SP - Brazil) soil.",
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AYZ62167; AAP86782.1; --
SEQUENCE 719 AA, 81216 MW; 3627E5A6C25DAFFS CRC64;
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100.0%; Pred. No. 2.6e-253;
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Bacillus thuringiensis.
Bacillus cereus group.
NCBI_TaxID=1428;
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02-MAR-2004 (TrEMBLrel. 27, Li
02-MAR-2004 (TrEMBLrel. 27, Li
Delta-endotoxin.
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                                                                   Query Match
Best Local Similarity 99.9
Matches 718; Conservative
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                                                                                                                                                      181 BEVPLLPIYAQAANLHILLILRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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                                                                                                                                                                                      EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                                  241 TGLNNLRGTNAESWVRYNOFRRDWTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI
                                                        RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSOYIALELMFVQKLPSFAVSG
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAZ-2004 (TrEMBLrel. 26, Last annotation update)
Insecticidal protein.
Name=cryV101;
Bacillus thuringiensis (subsp. kurstaki).
Plasmid large plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
11 TaxID=29339;
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databases
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HSSP; P02965; ICTY
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0006952; P:defense response; IEA.
InterPro; IPR00178; Endotoxin.
InterPro; IPR001878; Endotoxin.
InterPro; IPR008563; endotoxin.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin.
Pfam; PF03945; Endotoxin.
Pfa
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                                                                                   MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                    1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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81230 MW; 42746D478359BBA7 CRC64;
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Last sequence update)
Last annotation update)
                           Score 3754; DB 2;
Pred. No. 6.8e-253;
0; Mismatches 1;
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Bacillus thuringiensis (subsp. kurstaki).
Bacieria, Firmicutes, Bacillales, Bacillaceae,
Bacillus cereus group, Bacillus thuringiensis.
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                 RMEJ, AR278197; AAM73516.11.

RPIR, B4459; B42459.

RRSP; P02965; 1C17.

GO; GO:00005102; F:receptor binding; IEA.

GO; GO:0009405; F:receptor binding; IEA.

R GO; GO:0009405; F:pathogenesis; IEA.

RINEAPRO; IPRO0178; Endotoxin.

R InterPro; IPRO05638; endotoxin.

R InterPro; IPRO08979; Gal bind Tike.

R Ffam; PP03944; Endotoxin.

R Pfam; P703945; Endotoxin.M; 1.

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      the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              96.4%; Score 3625; DB 2; 96.2%; Pred. No. 6.7e-244; iive 12; Mismatches 15;
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Q970P8;
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     novel crylla-type gene
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                    CRC64;
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                                                                                               Score 3752; DB 2;
Pred. No. 9.4e-253;
1; Mismatches 1;
"Cloning and study of the expression of a novel Bacillus thuringlensis subsp. kurstaki."; J. Appl. Microbiol. 95:23-28(2003). EMBL, AJ31212, CASE5564.1; SEQUENCE 719 AA, 81203 MW; 8676E5A6C25DAFEB
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QBKY61;
01-0CT-2002 (TEMBLrel. 22,
01-0CT-2002 (TEMBLrel. 22,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                Local Similarity 99.7
1es 717; Conservative
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                                                                                                                                                                   PRT;
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PF00555; Endotoxin_M; 1.
PF03945; Endotoxin_N; 1.
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SEQUENCE 71
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                                                                                                                                   MEDIAINE-22837682; PubMed=12957903;
Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
Hu Y., Li G., Huang D.;
"Identification of cryll-type genes from Bacillus thuringiensis
strains and characterization of a novel cryll-type gene.";
Appl. Environ. Microbiol. 69:5207-5211(2003).
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                                                                                                                                                                                                                                                                                                                                                                            Length 719;
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                                                                       Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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   Created)
Last sequence update)
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93.6%; Pred. No. 9.7e-239;
ive 26; Mismatches 20;
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GO; GO: 0006912; P: defense response; IEA.
GO; GO: 00069405; P: pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008539; Gal bind like.
Pfam; PF03944; Endotoxin.C; 1.
Pfam; PF03945; Endotoxin.C; 1.
Pfam; PF03945; Endotoxin.M; 1.
Plasmid.
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EMBL; AF211190; AAG43526.1; -.
HSSP; P02965; 1CIY.
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Matches 673; Conservative
   01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                           Bacillus thuringiensis.
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                                                                     Plasmid pBTC19
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUD-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllb (Insecticidal delta-endotoxin Cryll(b)) (Crystaline entomocidal protoxin) (81 kDa crystal protein) Names-cryllb, Synonyms=cryllb, cryv, cryv465;
Bacillus thuringiensis (subsp. entomocidus).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl. Environ. Microbiol. 61:2402-2407(1995).

-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species. Active on Plutella xylostella but not on Bombyx mori.

-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99314293, PubMed=7793960, Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I., Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I., Instribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
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-	1	CC CC LEST		CC the Buy							KW Sporule	į	Query Matc Best Local		à a	۸۵	qu	Qy 12	ob 13		3t da	Qy 24	- da 24	36	)E	- Qy 36	9E	Oy 42	Db 42	Oy 48	Db 48	Qy 54	Db 54	09 XO	99 qu
	1 MKLKOVPDKHQSLSSNAKVDKIATDSLKNETDIELKONNNEDYLRMSEHESIDPFVSASTI 60	61 QTGIGIAGKIIGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA 120	RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQXIALELMFVQKLPSFAVSG 18	:  :	181 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240	181 BEVPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKMYN 240	241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300	241 TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI 300	301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNTQYMNW 360	301 GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNAM 360	361 GGHKLEFRTIGGTLNISTQGSTNISINPVTLPFISRDVYRTESLAGLNLFLTQPVNGVPR 420	361 GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGINLFLTQPVNGVPR 420	421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480	421 VDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480	481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN 540	TOTAL TOTAL STATE OF THE STATE	TOTICO IN THE TOTAL PROPERTY OF THE TOTAL PR	THE OFFICE AND THE STATE OF THE	601 TPRIIGETTESTESTESTESTESTESTESTESTESTESTESTESTE	TALETSTNPRGLKTDVKDVHIDOVSNIVESI.SDRFVI.DRKRELFRIVKVAKOIHIERNM 2	TALETSTRONG CHARLES SEEN TO CONTINUE STATE OF THE SEN THE SE	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	ISULT 10	CIID BACTU STANDARD; PRT; 719 AA.	16-OCT-2001 (Rel. 40, Created)	, ,	entomocidal protoxin) (81 kD	Bacillus thuringians. Bacillales Bacillaces Bacillus Rarreria Firmicutes.	sacillaida, bacillaccad, bacilla	SEUDINCE FROM N.A.	ر بر د	) of a new Bacillus thuringiensis cryll-type	4 6		-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
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SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation uropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way led and this statement is not removed. Usage by and for commercial les requires a license agreement (See http://www.isb-sib.ch/announce/nd an email to license@isb-sib.ch).
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he spore coat. ISCELLANEOUS: Toxic segment of the protein is located in the \ensuremath{\text{N}^-}
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PP: P02965; 1CIY.

erPro; IPRO0118; Endotoxin.

erPro; IPR005638; endotoxin.

erPro; IPR005639; endotoxin.

erPro; IPR005979; Gal bind like.

erPro; IPR005979; Gal bind like.

m; PP00555; Endotoxin. C; 1.

m; PP003945; Endotoxin. M; 1.

m; PP003945; Endotoxin. M; 1.

yurlation; Toxin. Toxin.

yUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
                                                   erminus.
IMILARITY: Belongs to the delta endotoxin family.
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InterPro; IPR001178; Endotoxin.
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Q45739;
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         TALFISINPRGLKIDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
                                  epithelial cells of insects.

DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
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                                                                                                                                                                                                    16-0c7-2001 (Rel. 40, Created)
16-0c7-2001 (Rel. 40, Last sequence update)
16-0c7-2001 (Rel. 44, Last sequence update)
Pesticidial crystal protein cryllc (Insecticidal delta-endotoxin
Cryll(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
Mame=cryllc; Synonyms=cryll(c);
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C18 / ESYPt,
OSMAN Y.A., MadKour M.A., Bulla J.A. Jr.;
Submitted (MAR.1998) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION; Promotes colloidosmotic lysis by binding to the midgut
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89.8%; Pred. No. 1.3e-226;
iive 33; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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or send an email to license@isb-sib.ch).
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InterPro; IPR001178; Endotoxin..
InterPro; IPR005638; endotoxin.C.
InterPro; IPR008639; endotoxin.N.
InterPro; IPR008879; Gal.bind_like.
Pfam; PF03944; Endotoxin.C; I.
Pfam; PF03945; Endotoxin.M; I.
Pfam; PF03945; Endotoxin.N; I.
                                                                                                                                                               PRT;
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                                                                                                                                                               STANDARD;
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30-MAY-2000 (Rel. 39, Last sequence update)
50-MAY-2000 (Rel. 44, Last annotation update)
65-JUL-2004 (Rel. 44, Last annotation update)
CTYLE (Additional Crystal protein crylBb (Insecticidal delta-endotoxin CTY1B(b)) (CTYStaline entomocidal protoxin) (140 kDa crystal protein).
Name-crylBb; Synonyms-crylB(b), cryET5;
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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24] IGLNNIRATNGQS#VRYNQFRKDIELMVLDLVRVFPSYDTLVYPIKTTSQLTREVYTDAI
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                                                                                                                    VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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STRAIN=NRE B.21110 / EGS847;
STRAIN=NRE B.21110 / EGS847;
Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins toxic to legidopteran insects.";
Patent number US5322687, 21-UUW-1994.
-:-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithalial cells of many lepidopteran larvae.
-:-PUNCTION: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the spore coat.
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HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
  Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                   65.1%; Score 2446.5; DB 1;
65.6%; Pred. No. 2.2e-161;
iive 92; Mismatches 138;
                                                                                                                                                                                                                                                                   HSSP, P02965; 1CIY.
InterPro; IPR00119; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008639; endotoxin.N.
InterPro; IPR00879; Gal.bind_like.
Pfam; PF00555; Endotoxin.M; I.
Pfam; PF03945; Endotoxin.M; I.
                                                                                                                                                                                                                                                       EMBL; Z46442; CAA86568.1; -. HSSP; P02965; ICIY.
                                                                                                                                                                                                                                                                                                                                                                                                         470; Conservative
                                                                                                                                                                                                                                                                                                                                                      Sporulation; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                               FROM N.A.
                         [1]
SEQUENCE
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
65-UTL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
CrylBlc)) (Crystaline encomocidal protoxin) (140 kDa crystal protein)
Name-crylBc; Synonyms-crylB(c), CrylBc;
Bacillus thuringiensis (subsp. morrisoni).
                                                                                                                                       SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIAGKI
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1229;
                                                                                                                  17;
                                                                                              Length
                             Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF0355; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
Sporulation; Toxin.
SEQUENCE 1229 AA; 139769 WW; A4C949DB675C3269 CRC64;
                                                                                                                  Indels
                                                                                            65.1%; Score 2446.5; DB 1; 65.6%; Pred. No. 2.2e-161; cive 92; Mismatches 138;
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IPR005638; endotoxin_C.
IPR005639; endotoxin_N.
IPR008979; Gal_bind_like.
                                                                                                                  Conservative
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                                                                                                       Similarity
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            InterPro;
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Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
                                                                                                                                                                                                           the spore coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                               epithelial cells of insects.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                terminus.
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543 535 603

483

663

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPI 359
                                                                                                                                                                                                                                                                                                                                                                                                SPECIES L.Kurstaki; STRAIN=HD-2;
SPECIES=B.L.Kurstaki; STRAIN=HD-2;
MEDLINE=88203216; PubMed=3362680;
Brizzard B.L., Whiteley H.R.;
"Nuclectide Sequence of an additional crystal protein gene cloned from
Bacillus thuringieness subsp. thuringiensis.";
Nucleic Acids Res. 16:2723-2723(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       delta-endotoxin
kDa crystal protein).
                                                                                                                                                                                                     417 TNPQNISDRGTANYSQP-YESPGLQLKDSETELPPETTERPNYESYSHRLSHIGIILQSR
                                                                                                                                                                                                                                                                                          VNVPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRTNTGG
                                                                                                                                                                                                                                                                                                                                                                 FGDIRVNINPPFAQRYRVRIRYASTIDLOFHISINGKAINQGNFSAIMNRGEDLDYKTFR
                                                    GGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLF--LTQPVNGVPRVDFHWKFV
                                                                                                360 GGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNF---
                                                                                                                                                         THP----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH
                                                                                                                                                                                                                                                            VKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 TVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISTNPRGLKIDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FININPRELKTOVIDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the midgut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- PUNELOPMENTAL STACE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the N-
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-!- MISCELLANEOUS: Toxic segment of the protein is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p05517; Q45731;

01-NOV-1988 (Rel. 3) Last sequence update)

01-FB-1996 (Rel. 3) Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

05-JUL-2004 (Rel. 44, Last annotation update)

05-JUL-2004 (Rel. 44, Last annotation update)

Pesticidial crystal protean cryla (Insecticidal delta-er

Cryla(a)) (Crystaline entomocidal protoxin) (140 kDa crylane-cryla) Synonyms-crylB(a), cryA4;

Bacillus thuringienesis (subsp. kurstaki), and

Bacillus thuringienesis (subsp. kurstaki), and

Bacillus thuringienesis (subsp. entomocidus).

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1228 AA
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SPECIES=B.t.entomocidus; STRAIN=HD-110;
Soetaert P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X06711; CAA29898.1; -. EMBL; X95704; CAA65003.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxiD=29339, 1436;
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P05517; Q45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGDSFRAYQQSLEDWLENKDDARTRSVLHTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
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                                                                                                                                                                                                                                                                                          LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
                                                                                                                                                                                                                                                                                                                           TFGDIRL/NINVPLSQRYRVRIRYASTTDLQFFTRINGTTVNIGNFSRTWARGDNLEYRSF
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                                                                                  TEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
                                                                                                                                                                                       RIVGFITIPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSNRKNENELINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKALTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 TDSLKNETDIELQNINH-------EDCLKMSEYENVEPFVSASTIQTGIAGKI
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SEQUENCE FROM N.A.

Mat Isa
Mat Isa
Mat Sal
Submitted (MAR-2001) to the EMBI/GenBank/DDBJ databases.

SUBMISTED (MAR-2001) to the EMBI/GenBank/DDBJ databases.

REMBL; AF363025; AAK51084.1; -...
HSSP; POT130; 1DLC.

GO; GO:0005102; F:receptor binding; IEA.

GO; GO:0005102; F:receptor binding; IEA.

GO; GO:000405; F:receptor binding; IEA.

GO; GO:000405; F:receptor binding; IEA.

InterPro; IRR005538; endotoxin.C.

InterPro; IRR005638; endotoxin.C.

InterPro; IRR005638; endotoxin.N.

InterPro; IRR005638; endotoxin.N.

InterPro; IRR005638; endotoxin.C.

IRR005648; Endotoxin.C; IRR005638; endotoxin.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=crylBa2;
Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Framicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
Delta-endotoxin CrylBa2.
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71 LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKALTDLKG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHÇVKWYSTGLNNLRGTN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:
|GDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AASWVRYNQFRRDLILGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGAT--GVNMA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMWGGHKLEFRTI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLF--LTQPVNGVPRVDFHWKFV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THP----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417 TNPQNISDRGTANYSQP-YESPGLQLKDSETELPPETTERPNYESYSHRLSHIGIILQSR 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKALVYSWIHRSADRINIIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGDILRRINIGT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFR 603
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                                                                                                                                                                                                                                                                                  23 TDSLKNETDIELQNINH-------EDCLKMSEYENVEPFVSASTIQTGIAGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKOLHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FININPRELETIOVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
                                                                                                                                                                                                Query Match 60.6%; Score 2277.5; DB 1; Length 1228; Best Local Similarity 62.7%; Pred. No. 1.3e-149; Matches 449; Conservative 80; Mismatches 162; Indels 25;
                                                                                                                                                     150 150 Y -> H (in strain HD-110).
1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;
                       InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008639; endotoxin.N.
InterPro; IPR0086399; Gal bind like.
Pfam; PF003944; Endotoxin.C; 1.
Pfam; PF00355; Endotoxin.M; 1.
Pfam; PF003945; Endotoxin.M; 1.
                                                                                                                                                     VARIANT
SEQUENCE
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Search completed: October 28, 2004, 18:29:51 Job time : 101.579 secs

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The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
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100.0%; Score 3760; DB 4; ilarity 100.0%; Pred. No. 1.1e-293; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 719; Conserva

Sequence 719 AA;

Length 719;

Warner SAJ

EA,

Mackay

Cayley PJ,

Carlile AJ, Lee MD;

Griffin J, Vincent JL,

(ZENE ) ZENECA LTD.

WPI; 2001-123015/13.

99GB-00015215.

29-JUN-1999;

Claim 14; Page 55-57; 72pp; English.

26 2446.5	65.1	1229	N	AAR54074	Aar54074 CryET5.
7 2446.	65.1	1229	~	AAW35259	20
8 2446.	65.1	1229	~	AAW17699	_
9 2446.	65.1	1229	0	AAW87633	
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1 2446.	65.1	1229	ω	ADK98479	_
2 2344.	N	488	7	AAW44322	
3 2344.	$\alpha$	488	4	AAB19947	_
4 2278.	0	1228	7	AAR50955	
5 2273.	0	1209	4	AAU02094	
6 2264.	0	1227	N	AAY31990	Aay31990 Chimeric
7 2195.	ω	1227	~	AAW44321	
8 2195.	α	1227	4	AAB19950	_
9 2186.	ω	1227	4	AAU02046	
0 2171.	~	1186	~	AAY16796	
1 2156.	~	1221	4	AAU00421	
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3 211	9	1228	4	AAB84628	ď
4 211	9	1228	4	AAU02039	
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RESULT 1					
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AC AAB66908;					
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Insecticidal	lal protein	ein crylla2	ııa;	2.	
KW Insecticide;		transgenic p	plant;	nt; insect-resistance.	
Paecilomyces	es sp.			-	
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XX PD 04-JAN-2001	1.				
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
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                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 3760; DB 6;
100.0%; Pred. No. 1.1e-293;
ive 0; Mismatches 0;
                                                                                                                  12; Page 44-47; 67pp; English
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Best Local Similarity 100.
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                                                                                       QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA
                                                                                                                                                                                                      EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                      TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYFIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                           MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
   MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insecticidal protein; pesticide; insecticidal crystal endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. thuringiensis insecticidal crystal endotoxin (CRY)
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Length 719;

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
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                                                                                                                                                        ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                     VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                        TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                       541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                             TERTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                        TFRIVGFTIPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                               VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                     ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
                                                                                                                                                                                                                                                                                                                                                                  TALFTSTNPRGLKTDVKDYHIDQVSNLVBSLSDBFYLDEKRELFBIVKYAKQLHIERNM
                                                                                                                                                                                                                                                                                                                                               TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. thuringiensis insecticidal crystal endotoxin (CRY)
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Pred. No. 2.3e-293;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 50-53; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is used in the invention
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larity 99.9%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYGN ) SYNGENTA LTD.
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Best Local Similarity
Matches 718; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTGIGLAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warner SAJ;
                                                                                                                                                                                     Insecticide; transgenic plant; insect-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mackay EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cayley PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 60-62; 72pp; English
                                                  Ä.
                                                standard; protein; 719
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99GB-00030536
                                                                                                                                                    protein crylla4
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                                                                                                                 (first entry)
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Matches 718; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carlile AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffin J, Carlile Vincent JL, Lee MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-123015/13
                                                                                                                                                                                                                                                                                                                                                                                                                (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 719 AA;
                                                                                                                                                                                                                     Paecilomyces sp.
                                                                                                                                                                                                                                                        WO200100841-A1.
                                                                                                                                                    Insecticidal
                                                                                                                                                                                                                                                                                                                                                            29-JUN-1999;
23-DEC-1999;
                                                                                                                   12-APR-2001
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                                              AAB66910
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New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is B. thuringiensis (Bt) crystal protein Crylla, the DNA encoding which was mutated to allow cloning of domain II or domains I and II, to make the hybrid protoxins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.9%; Pred. No. 5.8e-293;
Matches 718; Conservative 0; Mismatches 1.
                                                                          (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD
                                                                                                                                                                                                                                       Page 30-32; 43pp; English.
                         99EP-00203723
                                                    99EP-00203723
                                                                                                                                WPI; 2001-337141/36.
N-PSDB; AAS04855.
                                                                                                        Bosch
                                                                                                                                                                                                                                                                                                                                                                         Sequence 719 AA;
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                          09-NOV-1999;
                                                    6661-VON-60
16-MAY-2001
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                                Bacillus thuringiensis partial mutant Crylla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crylla5.
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    TGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREVYTDAI
                                                           GTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFLBQVTIYSLLSRWSNTQYMNWW
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Lee MD;
                                                                                                                                                                                                                                                                                                          (first
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Best Local Similarity
Matches 716; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Paecilomyces sp.
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                                                                                                                                                                                                                                                                                                                                                     Insecticidal
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Vincent JL,
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ABE 659
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                                                       99GB-00015215
99GB-00030536
                                                                                                                                                                                                                                                                                          Local Similarity 99.6
Hes 716; Conservative
                                                                                                    Carlile AJ,
                                                                                                                                                            controlling insects,
                                                                                                              Lee MD
                                                                                                                                WPI; 2001-123015/13.
                                                                                                                                                   insecticidal
                                                                                   (ZENE ) ZENECA LTD
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  WO200100841-A1
                                       23-JUN-2000;
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23-DEC-1999;
                                                                                                   Griffin J,
Vincent JL,
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                                                                                                          MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                      RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSG
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                                                                                             MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                           Gaps
other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. sequence is used in the invention
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                                                         Length 719;
                                                                          Indels
                                                        Score 3749; DB 6;
Pred. No. 8.4e-293;
2; Mismatches 1;
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Local Similarity 99.6%;
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QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWBIFMEHVEBIINQKISTYA 120
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                                                                                                                                                                                   protein obtained from species of Paecilomyces, and for insect-resistant transgenic plant
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SAJ;
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Warner
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Pred. No. 2.5e-292;
1; Mismatches 2;
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GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360
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                                                                                                                                                                                                          VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
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                                              GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis strains – used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.
                              TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 kD endotoxin deduced from DNA carried on pJH12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crystal; insecticide; toxin; delta endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis; JHCC 4353 and 4835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR08041 standard; protein; 719 AA
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27-FEB-1991
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                                                                                          661 TALFISINPRGLKTDVKDYHIDQVSNLVESLSDBFYLDEKRELFEIVKYANELHIERNM 719
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                   TFRTVGFTTPFSFLDVQSTFT1GAWNFSSGNEVYIDR1EFVPVEVTYEAEYDFEKAQEKV
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                                                                                                                                                                                                                                                                                                   Insecticidal protein, pesticide, insecticidal crystal endotoxin, CRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insecticidal protein comprising an X-glycine motif at the aminoterminus, useful as an active ingredient of a pesticide.
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Pred. No. 2.5e-292;
1; Mismatches 2;
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                                                                                                                                                                                 AAE36273 standard; protein; 719 AA
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be used to produce transformants B.coli strain MC12022/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-WAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                                                   Score 3739; DB 2;
Pred. No. 5.3e-292;
; Mismatches 3;
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Best Local Similarity 99.6
Matches 716; Conservative
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terminus, useful as an active ingredient of a pesticide.
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Pred. No. 3.7e-291;
); Mismatches 2;
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Best Local Similarity 99.6'
Matches 716; Conservative
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                                                                                                                                                  (SYGN ) SYNGENTA LTD
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GRY

Insecticidal protein; pesticide; insecticidal crystal endotoxin;

B. thuringiensis insecticidal crystal endotoxin (CRY) protein,

(first entry)

26-JUN-2003

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standard, protein; 718

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                                                                                                                                                                                                                                                                                                                                                                                                                               TALFTSINPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
            TERIVGETIPESFLDVQSIFTIGAMNESSGNEVYIDRIBEVPVEVIYSBABYDFEKAQEKV
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                                                                                                                                                                  361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
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                                                TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                            GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMM
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crylle1.
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N-PSDB; ADM74716.
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                   TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
                                                 TFRIVGFITPFSFLDVQSTFIIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 660
                                                                    TERTVGFTTPFSLLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 659
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                                                                                                                            718
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                                                                                                 Gaps
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Pred. No. 1.1e-290;
0; Mismatches 3;
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Lee MD;
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Best Local Similarity
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Vincent JL,
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        The invention relates to a novel Bacillus thuringiensis cryl gene, gene combination, expression vector, nucleotide sequence of the B thuringiensis cryl gene with high-toxicity to lepidoptera pests and the amino acid sequence of the protein encoded by it, cooperative use of the cryl gene with the expression product of crylAb or crylBa, primer sequences for expressing the genes, and the constructed shuttle vector pSX412b. The gene in combination with the crylAb or crylBa genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the crylIel protein.
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94.4%; Score 3551; DB 7;
Best Local Similarity 93.6%; Pred. No. 7.5e-277;
Matches 673; Conservative 26; Mismatches 20;
                                                                                                                                     Sequence 719 AA;
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standard; protein;

RESULT 14
AAB66912
ID AAB66912 s
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AC AAB66912;
XX
DT 12-APR-200

(first entry)

12-APR-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel insecticidal proteins obtained from Paccilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
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                                                                                                                                                                                                                                                                                                                                                                                Novel insecticidal protein obtained from species of Paecilomych controlling insects, and for insect-resistant transgenic plant
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92.9%; Pred. No. 2.4e-274;
ive 31; Mismatches 20;
                                 Insecticide, transgenic plant, insect-resistance.
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                                                                                                                                                                                                                                                                                             Mackay
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                                                                                                                                                                                                                                                                                              Cayley
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                                                                                                                                                                        23-JUN-2000; 2000WO-GB002457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668; Conservative
                                                                                                                                                                                                                                                                                              ΑĊ,
                                                                                                                                                                                                                                                                                             Carlile Lee MD;
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                                                                                                                                                                                                                                                           ZENE ) ZENECA LTD
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                                                                    Paecilomyces sp.
                                                                                                     WO200100841-A1.
Insecticidal
                                                                                                                                                                                                         29-JUN-1999;
                                                                                                                                     04-JAN-2001
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Vincent JL,
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynuclectide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or smegistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiens insecticidal crivity are present sequence is sequence is used in the invention
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                                                                                                                                                                                                                                                                                                     ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
                                                                                                                                                                                                                                                                 TPRIVGETIPESFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV
ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; pesticide; insecticidal crystal endotoxin; CRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
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        VDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS
                               EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSDHCVKWYS
                                                                                                                                         VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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Search completed: October 28, 2004, 18:19:54 Job time : 95.6903 secs

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Gaps

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93.6%; Score 3520; DB 6; Length 719; 92.9%; Pred. No. 2.4e-274; rive 31; Mismatches 20; Indels

Query Match Best Local Similarity 92.9% Matches 668; Conservative

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Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

ALIGNMENTS

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence

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CLILE
STATE: D.
COUNTRY: USA
ZIP: 20005-3918
ZIP: 20005-3918
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-MUG-1994
CLASSIFICATION ATA:
APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1990
APPLICATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
RESERBENCE COCKET NUMBER: 70608/220720
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08286870A

Patent No. 60636AE

GENERAL INFORMATION:
APPLICANT: TATLOR, RH
APPLICANT: TATLOR, RH
APPLICANT: TATLOR, RH
APPLICANT: TATLOR, RH
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Intellectual Property Group of
ADDRESSER: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
                                                                                                US-09-661-322A-6
US-07-876-280-30
US-07-876-280-30
US-08-315-468-2
US-08-315-468-2
US-08-357-999-2
US-08-375-999-2
US-08-379-658-5
US-08-471-177-5
US-09-411-177-5
US-09-411-1
                  US-09-178-252-25
US-09-826-660-25
PCT-US91-02560-4
                  RESULT:1
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-116-865-4

US-08-170-046-4

US-08-170-046-4

US-08-801-340-4

US-08-961-803-10

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                                                                                                           Length 710;
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92.5%; Score 3476.5; DB 4;
Best Local Similarity 92.5%; Pred. No. 5.2e-303;
Matches 665; Conservative 15; Mismatches 30;
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 ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)...(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
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Patent No. 605362...
GENERAL INFORMATION:
APPLICANT: ELY, S.
APPLICANT: TRILOR, HH
APPLICANT: TRIPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amr J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT APPLICATION NOWBER: US/09/661,322A
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
SEQ ID NO 42
LENGTH: 710
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                                                                  MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
                                     Gaps
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      Length 719,
                                     Indels
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        DB 3;
    Score 3756; DE;
Pred. No. 0;
1; Mismatches
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Patent No. 6593293
GENERAL INFORMATION:
        99.09
99.09
Query Match
Best Local Similarity 99.9°
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US-09-661-322A-42
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  481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
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                                                                                                                                   541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
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                                481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                             541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
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                                                                                                                                                                                                                       Query Match

89.8%; Score 3377; DB 2; Length 719;
Best Local Similarity 89.8%; Pred. No. 4.6e-294;
Matches 646; Conservative 33; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: Maddour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                           601 TERTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYE
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09003217
Patent No. 5986177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,943
REPERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray.
REGISTRATION NUMBER: 32,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
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CITY: Raleigh
STATE: NC
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US-09-003-217-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MB-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
-FILING DATE: 05-MG-1994
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: 18 07/52028
FILING DATE: 09-MAY-1989
ATPARAZ/AGENT INFORMATION:
NAME: PADLICATION NUMBER: 16,773
REGISTRANICATION NUMBER: 16,773
REGISTRANICATION NUMBER: 16,773
REGISTRANICATION NUMBER: 16,773
REGISTRANICATION NUMBER: 16,773
RELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: CASO 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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100.0%; Pred. No. 5e-296;
iive 0; Mismatches 0;
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLD
STREET: 1100 New York Avenue, N.W.
CITY: Washington
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Best Local Similarity 100.0
Matches 648; Conservative
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MOLECULE TYPE: protein
US-08-286-870A-4
                                                                              CLAL
CLATTE: DC
COUNTRY: USA
TP: 20005-3918
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	7 7	RESULT 6 US-08-286-870A-6  US-08-286-870A-6  Sequence 6, Application US/08286870A  Patent No. 6053605  APPLICANT: ELY, S  APPLICANT: TATLOR, RH  APPLICANT: TIPPER, RG  TITLE OF INVENTION: BACTERIAL GENES  NUMBER OF SEQUENCES: 10  CORRESPONDENCE ADDRESS: 1  ADDRESSEE: Intellectual Property Group of  ADDRESSEE: Intellectual Property Group of  ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  STREET: 1100 New York Avenue, N.W.  CITY: Washington  STATE: DC  COUNTRY: USA	COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM FC compatible  COMPUTER: TBM FC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  PRIOR APPLICATION NUMBER: US 07/52028  PRIOR APPLICATION NUMBER: US 07/52028  PRIOR APPLICATION NUMBER: US 07/52028  PRIOR APPLICATION NUMBER: GB 8910624.9  FILING DATE: 09-MAY-1989  PRIOR APPLICATION DATA:  APPLICATION NUMBER: GB 8910624.9
181 BEVPLLPIYAQAANLHLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWNN 240 241 TGLNNLRGTNAESWVRYNQFREDMTLMYLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300 241 TGLNNLRATNGGSWVRYNQFRKDIELWYLDLVRVFPSYDTGWYPIKTTAQLTREVYTDAI 300 241 TGLNNLRATNGGSWVRYNQFRKDIELWYLDLVRVFPSYDTGWYPIKTTSQLTREVYTDAI 300 301 GTVDPHDESTTSTTWYNNNAPSFSAIEAAVVRAPHLLDFLEKVTIYSLLSRWSNTQYMNWM 360 41 GGHKLEFRIGGTLANISTQGSTNTSINPYLLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420 421 GGHKLESRPIGGALNTSTQGSTNTSINPVTLQPTSRDFYRTESWAGLNLFLTQPVNGVPR 420 421 VDFHWKFPTHPIASDNFYYPGYAGIGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTHPIASDNFYYPGYAGIGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPTASDNFYYPGYAGIGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPTASDNFYYLGYAGVGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPTASDNFYYLGYAGVGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPTASDNFYYLGYAGVGTGTQLQDSENBLPPEATGQPNYESYSHRLSHIGLIS 540 421 TGTFGHIRNNINPFRADRITNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDLLRRTK 540 541 TGTFGHIRVNINPPFAQRYRVRNSYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600 541 GGFFGHIRVNINPPFAQRYRVRNSYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600	601 TERTVGFTTPESFLDVQSTFTIGAWNFSSGNEVYIDEIEFVPVEVTYBAEYDFEKAQEKV 660	Gequence 2, Application US/09218942 Faceria No. 632439 GENERAL INFORMATION GENERAL INFORMATION: Bacillus Thuringiensis Isolates with Broad Spectrum TITLE OF INVENTION: Activity TITLE OF INVENTION: Activity TITLE OF INVENTION: Activity CURRENT PEDILCATION NUMBER: US/09/218,942 CURRENT PEDILCATION NUMBER: 05/035,361 EARLIER PELING DATE: 1997-01-10 EARLIER PELING DATE: 1998-01-06 EARLIER FILING DATE: 1998-01-06 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NOS: 2 SEQ ID NO 2 LENGTH: 719 TYPE: PRI ORGANISM: Bacillus thuringiensis	Query Match         89.7%;         Score 3372;         DB 3;         Length 719;           Best Local Similarity         89.8%;         Pred. No. 1.3e-293;         0;         Gaps         0;           Matches         646;         Conservative         33;         Mismatches         40;         Indels         0;         Gaps         0;           1         MKLKNOPKHQSFSSNAKVDKISTGELGELWENDHEDCLKMSEVENUEPFVSASTI         60         61         INTERNETGILGTLGVPPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEINQKISTYA         120         61         OTGIGIAGKILGTLGVPPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEINNCKISTYA         120         121         RNXALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVG         180           121         RNXALTDLKGLGDALAVYHESLESWVGNRNNTRARSVVKNQYIALELMFVQKLPSFAVG         180           121         RNXALTDLKGLGDALAVYHESLESWVGNRNNTRARSVVKNQYIALELMFVQKLPSFAVG         180

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423 --INPONIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLIIGN 480
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                                   Conservative
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 Pennsylvania
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APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Jan, Christine S.
APPLICANT: Jan, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: PACILLUS THURINGIENSIS CRYETY AND CRY!
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPINUMBER OF SEQUENCES: S.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
                                                       70608/220720
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Patent No. 5322687
GENERAL INFORMATION:
           NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 7060/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             Best_Local Similarity 100.
Matches 535; Conservative
                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-286-870A-6
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US-08-100-709-4
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REGISTRATION NUMBER: 27633
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TELECOMOUNICATION:
TELEPHONE: 216-757-1590
INFORMATION FOR SEQ ID NO: 4:
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Batent No. 5616319

GENERAL INFORMATION:
APPLICANT:
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Genzalez Jr., Jose M.
TITLE OF INVENTION: BACTILLUS THURINGIENSIS CTYET4 AND CTYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel Control of the bottom 
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                                                         NENEINALSIPTVSNPSTQMYLSPDARIEDSLCVAEVNNIDPFVSASTVQTGINIAGRI
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                                  LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
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65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.7e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

FILLING DATE: 30-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-176-865-4
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APPLICANT: DONOVAIN, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Consalez V. Jose M.
TITLE OF INVENTION: DACILLUS THURINGIENSIS CTYET4 AND CTYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
TORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CTY: Philadelphia
STATE: Pennsylvania
CCUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602
STIWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLEFRII 370
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                                         307 STWWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHRLNFRPI
                                                                                                                                                                      367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF----
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                                                                                                                                GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT
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247 AESWIRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRTNAPSGFA 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGINILFTTPVNGVPWARFNF--- 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGLAGKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.1%; Score 2446.5; DB 2; Length
65.6%; Pred. No. 3.7e-210;
tive 92; Mismatches 138; Indels
 ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOIS, CARISTOPHER: REGISTRALION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                 Philadelphia
: Pennsylvania
RY: U.S.A.
                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                     1601 Market
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Best Local Similarity
Matches 470; Conservat
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                     ADDRESSEE:
STREET: 16
CITY: Phil
STATE: Per
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Patent No. 5854053

GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --INPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLIIGN 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STTWYNNNAPSFSAIEAAVVRNPHILDFLEQVTIYSLLSRWSNTQYMNWGGHKLEFRTI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPRVDFHWKFVT 429
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                                                                                                                                                                                  13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGLAGKI
                                                                                                                                                      17;
                                                                                                                    Length 1229;
                                                                                                                 65.1%; Score 2446.5; DB 1; Length
65.6%; Pred. No. 3.7e-210;
ive 92; Mismatches 138; Indels
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4
                                                                                                                                                    Conservative
                                                                                                                                    Similarity
                                                                                                                                                  470;
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US-08-779-046-4
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                                                                                                                   Query Match
Best Local
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Genes
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APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Statman, Steve
APPLICANT: Statman, Steve
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and TITLE OF INVENTION: Bncoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
                                                                                              251 AESWVRYNQFRRDMTLMVLDLVALFPSYDTQNYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
                                                                                                                                                                                                                                                                                                                        423 --INPONIYERGATTYSOPYOGVGIÓLFDSETELPPETTERPNYESYSHRLSHIGLIIGN 480
                                                                                                                                                                                                                                                                                                                                                          542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTAGESTPFNFLNAGSTFTLGAGSFSN-QEVYIDRVEFVPAEVTFEAEYDLERAQKAVNA 659
                                                                                                                  247 AESWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDFIGRTNAFSGFA 306
                                                                                                                                                                                                                                                482
127 LGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186
                                                                                                                                                                                                                             GGTLNISTOGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 ILRAPVYSWTHRSADRINTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRINTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA
                                                      HVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTG
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                                                                                                                                                                 STIWYNNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNTQYMNMWGGHKLEFRTI
                                                                                                                                                                                       430 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS
                                    OAANLHLLLLRDASI FGKEWGLSSSEI STFYNRQVERAGDYSDHCVKWY STGLNNLRGŢN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                           Sequence 4, Application US/08881340

Patent No. 5942658

GENERAL INPORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: S.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGTLGVPFAGOVASLYSFILGELWPKGKNOWEIFMEHVEEIINQKISTYARNKALTDLKG 130
                                       900
                                                                        662
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                                                                                                                                     LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
                                                                                                                                                        543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
                         67 LGVLGVPPAGOLASFYSFLVGELWPSGRDPWEIFLEHVEQLÍROOVTENTRNTALARLEG
                                                                        603 RIVGFIIPFSFLDVQSIFIIGAMNFSSGNEVYIDRIEFVPVEVIYEAEYDFEKAQEKVIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.1%; Score 2446.5; DB 2; Length 1229; 65.6%; Pred. No. 3.7e-210; ive 92; Mismatches 138; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 1601 Market Street, 36th Floor
Philadelphia
Pennsylvania
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.6
Matches 470; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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US-08-881-340-4
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172 EEVPLLPIYAQAANLHLLLRDASIFGKKWGLSDSEISTFYNRQSGKSKEYSDHCVKWYN 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTVHPHPSFTSTTWYNNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RNKALIDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 IGINRIMGNNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKNSEYBNVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Gaps
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                                                                                                                                                                                                                                                                              SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILLIG DATE: 31-OCT-1997
CLASSIFICATION .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%; Score 2344.5; DB 3;
89.7%; Pred. No. 1.2e-201;
ive 13; Mismatches 29;
                                                                                                 Suite
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-UNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-4AY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                AUDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street,
CITY: Galnesville
STATE: Florida
COUTRY: USA
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: M/S
TELECOMMUNICATION INFORMATION:
TELEFAHOR: (352) 375-8100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sanders, Jay M. REGISTRATION NUMBER: 39,355
     Encoding
10
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Matches 446; Conservative
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                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sa
     OF INVENTION:
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Ratent No. 6150589

GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cannoin, Raymond J.C.
APPLICANT: Cannoin, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Steve
TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTGIGIVGKILGNLGVPFAGQVASLYSFILGELWPKGKSQWEIFWEHVEELINQKISTYA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNKALADLKGLGDALAVYHESLESWIENRNNTRTRSVVKSQYITLELMFVQSLPSFAVSG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 TGLNRLMGNNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 471
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89.7%; Pred. No. 1.2e-201;
iive 13; Mismatches 29; 1
                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERRUCE/DOCKET NUMBER: M/S 102D.C1
TELEPHONE: (904) 375-8100
TELEFAX: (904) 375-8100
TELEFAX: (904) 372-500
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LINGTH: 488 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
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Best Local Similarity 89.7%,
Matches 446; Conservative
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US-08-961-803-10
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                                                                                                                                                                                           SOYIALBLMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIST 219
                                                                                                                                                                                                                ENELPPEATGOPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITOIPL 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 FYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYD 279
                                                                                                                                                                                                                                                                                                                            280 TOMYPIKTTAQLIREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFL 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHISINGKAINQGNESATMARGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAMNFSSGNE 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 FPVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSGNGE 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS 692
                                                        40 EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKN
                                                                             10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVFGAGQLASFYSFLVGELWFRGRD
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                          Indels
          Pred. No. 6.3e-194;
; Mismatches 154;
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US-08-459-448A-7
US-08-d59-448A-7
Sequence 7, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
64.3%; Pies
78;
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Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
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Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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Bowman, Cindy G.
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Suttie, Janet L.
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r, Erik M.
Gary M.
          Best Local Similarity 64,3
Matches 442; Conservative
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                                                                                             VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill: W W.......
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7.Skyline Drive
                                                                                                                                                                                                                                                                              Sequence 7, Application US/07951715A Patent No. 5625136
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Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
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Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola Stephory W.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
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REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION:
TELEPHONE: (919)541-8615
                                                                                                                                                                                      ASHVKALVYSWTHRSAD 488
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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STATE: New York
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US-07-951-715A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQVIIYSLLSRWSNTQYMNWWGGHKLEPRTIGGTLNISTQGSTNTSINPVTLPFTSRDVY 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QWEIFWEHVEEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRIYPINTSAQLTREVYTDAIGAT--GVNMASMWWYNNNAPSFSAIEAAAIRSPHLLDFL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKN 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                               SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.3%; Score 2265.5; DB 2; Length Best Local Similarity 64.3%; Pred. No. 6.3e-194; Matches 442; Conservative 78; Mismatches 154; Indels
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENH.
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tartytown
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY,AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REPERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELEPHONE: (919)541-8582
TELEPHONE: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                          ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1207 amino acid
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43; Search time 19:191 Seconds
(without alignments)
3604.811 Million cell updates/sec
Title: US-10-019-823B-55
Perfect score: 3760
Sequence: 1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYAKQLHIERNM 719
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 283416

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	al prot	ü	cida]	cryV465 protein -	1	hypothetical prote	l cz	ᅼ		ᅼ	ᅼ		1 crysta	parasporal crystal	4	o T	겁	ᅼ	о П	-	-	٦.	ď	d	asporal c	al	asporal	arasporal crysta	arasporal c
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Length	719	719	719	719	1228	380	15	16	15	1174	15	15	934	17	15	18	17	15	17	1176	17	13	15	823	18	15	1171	17	17
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Score	376	75	3743	52	۲.	90	Q)	ų,	47	1471	46	46	54.	453.	S	1449.5	447.	4	٠	443.	36	35	339.	Η.	322.	31	1272	27	26
Result No.		7	٣	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

parasporal crystal	_	protoxin - Bacillu	parasporal crystal												
S32647	S11446	JC7140	532689	I40589	USBSXH	A49785	A27323	S10228	139811	JH0261	S11445	S19306	USBSBI	B29838	139870
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32.8 1160 2	0	655 2	1172 2							26.2 649 1		1			-1
1234 32.8 1160 2	0	32.2 655 2	31.8 1172 2		30.9	30.9	30.7	30.1	29.3		24.9	1		18.5	17.7 1

## ALIGNMENTS

	RESULT 1	
	I39815	
	insectic	insecticidal protein cryv - Bacilius Churingiensis
	C, specie	Cibbecies: bactiling cintringienibits Cibate: 19-111-1904 Heemience revision 19-1111-1996 Hrext Chande 09-1111-2004
	C, Access	
	R,Gleave	R;Gleave, A.P.; Williams, R.; Hedges, R.J.
	Appl. En	Appl. BIVIION MICEODIOL 34 - 6841-6861, 1993 A. THITE: Greening by nollymerase chain reaction of Bacillus thuringiensis serctiones for t
	iensis s	
	A;Refere	A.Reference number: 139815; MUID:93298009; PMID:8517758
	A;Status	#Arcession: 1994.) A.Status: Drelininary: translated from GB/EMBL/DDBJ
	A; Molecu	A; Molecule type: DNA
	A,Residu	A;Residues: 1-719 <res> 2.rross-references: INTPROT-045752; GR:M9R544: NID:d142767; PIDN:AAA22354.1: PID:d142768</res>
	C;Genetics:	11
	A;Gene: C;Superf	A;Gene: cryV C;Superfamily: parasporal crystal protein
	Query	Query Match 100-08:; Score 3760; DB 2; Length 719;
	Best Loo Matches	ative 0,
	δλ	1 MKLKNODKHOSFSSNAKUDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 60
	qq	
	δ	61 QTGIGLAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYA 120
	qa	61 QTG1G1AGKILGTLGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYA 120
	ò	121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
	qq	121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
	ò	181 BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
	qa	181 BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
	ò	241 TGLNNLRGINAESWVRYNQFRRDWILMVLDLVALFPSYDTQWYDIKTTAQLTREVYTDAI 300
	qq	241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300
	'n	301 GTVHPHPSFISTTWYNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
•••	QQ	301 GTVHPHPBSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEGVTIYSLLSRWSNTQYMNWW 360
	λo	361 GGHKLEFRIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLIQPVNGVPR 420
	đđ	361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

Qy 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSBNELPPBATGQPNYESYSHRLGHIGLI	1	Qy 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	QY 601 TERTVGFTTPPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV	QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM	RESULT 3 139814 insecticidal protein cryV1 - Bacillus thurifications: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Date: 19-Jul-1996 #sequence_revision 19-J C;Accession: 139814 R;Shin, B.S.; Park, S.H.; Choi, S.K.; Kco, Appl. Environ. Microbiol. 61, 2402-2407, 19 A;Title: Distribution of cryV-type insectic comocidus. A;Reference number: 139814; MUID:95314293; A;Reseatues: preliminary; translated from GB/E A;Molecule type: DNB A;Residues: 1-719 eRES A;Cross-references: GB:L36338; NID:9540281; C;Genetics: A;Genetics: C;Superfamily: parasporal crystal protein	Query Match 99.5%; Score 3743; DB 2; Length 719; Best Local Similarity 99.6%; Pred. No. 4.6e-255; Matches 716; Conservative 1; Mismatches 2; Indels 0; Gap:	QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEFFVSASTI	OY 61 QTGIGIAGKILGTLGVPFAGQVASLYSPILGELWPKGKNOWBIFWEHVEBIINQKISTYA	QY 121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG	Qy 181 EEVPLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDVSDHCVKWYS	Qy 241 TGLNNLRGTNAESWVRYNOFRRDMTLAVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI	Qy 301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSFWSNTQYMNWM
THPIASDNFYYPGYAGIGTQLQDSENELPPEATGG	YYPGYAGI RTNTIEPN	CY 541 TGTPGDIRVNINPPFAQRYRURIRYASTTDLOFHTSINGKAINQGNFSATMARGEDLDYK 600 	QY 601 TERTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIBFVPVEVTYBABYDFBKAQEKV 660	QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVBSLSDBFYLDBRRBLFBIVKYAKQLHIBRNM 719 	RESULT 2 82538  Sarasporal crystal protein crylIal - Bacillus thuringiensis  Darasporal crystal protein crylIal - Bacillus thuringiensis  NiAlternate names: delta-endotoxin; parasporal crystal protein cryV  C;Species: Bacillus thuringiensis  C;Date: 17-Apra-1923 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004  C;Accession: S25383 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004  R;Tallor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  Morcobiol. 6, 1211-1217, 1952  A;Reference number: S25383; MUID:92269582; PMID:1588820  A;Accession: S25383  A;Molecule type: DNA  A;Residues: 1-719 <tal: a;cross-references:="" a;genetics:="" c;cuperfamily:="" c;genetics:="" c;keywords:="" crystal="" delta-endotoxin<="" embl:x62821;="" nid:g40289;="" parasporal="" pid:g4029="" pidn:caa44633.1;="" protein="" td="" uniprot:q45752;=""><td>Query Match Best Local Similarity 99.9%; Pred. No. 1.3e-255; Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</td><td>QY 1 MKLKONODKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 60                                    </td><td>QY 61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYA 120                                      </td><td>QY 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 Db 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180</td><td>Qy 181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240                                      </td><td>OY 241 TGLNNLRGTNAESWVRYNQFRRDWTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300  </td><td>QY 301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNFHLLDFLEQVTIYSLLSRWSNTQYMNWW 360                                      </td></tal:>	Query Match Best Local Similarity 99.9%; Pred. No. 1.3e-255; Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	QY 1 MKLKONODKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 60	QY 61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYA 120	QY 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 Db 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180	Qy 181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240	OY 241 TGLNNLRGTNAESWVRYNQFRRDWTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300 	QY 301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNFHLLDFLEQVTIYSLLSRWSNTQYMNWW 360

& a	421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQQPNYESYSHRLSHIGLIS 480	QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
os os	481 ASHVKALVYSWTHRSADRINIEPNSITQIPLVKAFNLSSGAAVYRGPGFTGGDILRRIN 540	QY 481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN 540
Sy Op Op	541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMYRGEDLDYK 600	QY 541 TGTEGDIRVNINEPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600 
ري 19	601 TERTVGETTPESFLDVQSTFTIGAMNESSGNEVYIDRIEFVPVEVTYZAEYDFEKAQEKV 660	Qy 601 TERTUGETTPESFLDVQSTFTIGAMNFSSGNEVYIDRIBEVPVEVTYEAEYDFEKAQEKV 660 
oy Dp	661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESISDEFYLDEKRELFEIVKYAKQLHIERNM 719 	Qy 661 TALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERMM 719 
RESULT , 140590 cryV465 C; Specie C; Acces C; Shin, R; Shin,	RESULT 4 140590 cryV465 protein - Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004 C;Accession: 140590 R;Shin, B.S., Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.	RESULT 5 \$00877 \$00872 parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis N;Alternate names: parasporal crystal protein cryA4 C;Species: Bacillus thuringiensis subsp. thuringiensis C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: \$00873
Appl. E A,Title tomocid A,Refer A,Acces	es in B	R;Brizzard, B.L.; Whiteley, H.R. Nucleic Acids Res. 16, 2723-2724, 1988 A;Tile: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t A;Reference number: S00873; WUID:88203216; PMID:3362680 A;Accession: S00873.
A, Statu A, Molec A, Resid A, Cross C, Genet	ls: preliminary; translated from GB/EMBL/DDBJ luch type: DNA lucs: 1-719 <res> -references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; FIDN:AAA82114.1; FID:g4672 ics:</res>	A;Molecule type: DNA A;Residues: 1-1228 <bri> A;Residues: 1-1228 <bri> A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g580949 C;Genetics: A;Gene: cryA4</bri></bri>
A;Gene: C;Super	cryv465 family: parasporal crystal protein	A;Start codon: TTG C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin
Query Best Match	Query Match 93.6%; Score 3520; DB 2; Length 719; Best Local Similarity 92.3%; Pred. No. 2.2e-239; Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;	Query Match 60.6%; Score 2277.5; DB 2; Length 1228; Best Local Similarity 62.7%; Pred. No. 1.2e-151; Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;
Sy B	1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEVENVEPFVSASTI 60	TDSLKNETDIELQNINHEDCLKMSRYENVEPFVSASTIQTGIGIAGKI 70
Oy Dp	OTGIGIAGKILGTLGVPPAGQVASLYSFILGELWPKGKNOWEIFMEHVEEIINQKISTYA 1 	71 LGTLGVPFACQVASLYSFILGELMPKGKNQWEIFWEHVEBIINQKISTYARNKALTDLKG 
S d	SFAVSG	Qy 131 LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYA 190 
oy Oy	181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240	
& a	241 TGLNNLRGINAESWYRYNOFRRDWILMYLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI 300 241 TGLNNLRGINAKSWYRYNOFRKDWILMYLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI 300	
oy Op	301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW 360	311
\$ 93 25	361 GGHKLEFRTIGGTLNISTOGSTNTSINPVTLFFTSRDVYRTBSLAGLNLFITQPVNGVPR 420	371 GGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFV
		Db 360 GGGINTSTHGAINTSINFVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVFTVRFNF 416

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26 LKNETDIELQNINHEDCLKMSEYENVEPFVSAS-
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B4459
hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (fr
C;Gpecies: Bacillus thuringiensis
C;Dpecies: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: B42459
B;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C
J. Bacteriol. 173, 3966-3976, 1991
A;Atleferonce number: A42459; MUID:91286178; PMID:2061280
A;Accession: B42459
A;Cross_references: UNIRROT:08KY61; UNIPROT:Q45740; GB:M63897
C;Superfamily: parasporal crystal protein
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               TNPQNISDRGTANYSQP-YESPGLQLKDSETELPPETTERPNYESYSHRLSHIGIILQSR
                                                VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT
                                                                       VNVPVYSWTHRSADRINTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRINTGG
                                                                                                    FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFR
                                                                                                                                                     TVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTAL
                                                                                                                                                                                                        FISTNPRGLKTDVKDYHIDQVSNLVBSLSDBFYLDEKRELFEIVKYAKQLHIERNM 719
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8; Mismatches 9;
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Best Local Similarity 95.5%;
Matches 363; Conservative
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RESULT

parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIH
S;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: A59350; 849247
R;Alambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V& Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity again A;Reference number: A59350; MUID:96141404; PMID:8572715
A;Accession: A59350
A;Molecule type: DNA
A;Residence contact to MINFOT:Q45733; EMBL:Z37527; NID:g547554; PIDN:CAA85764.1; PID:g54755
A;Experimental source: serovar tolworthi
C;Superfamily: parasporal crystal protein, active against corn borer and other insects, C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin PIDN:CAA85764.1; PID:954755 other insects, 137 148 197 328 366 386 420 429 470 469 589 635 DRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEF 695 208 257 268 317 521 529 581 78 88 AGQVASLYSFILGELWPKGKNQ-WEIFWEHVEELINQKISTYARNKALTDLKGLGDALAV SGQIVSFYQFLLNTLWPVNDTAIWEAFMRQVEELVNQQITEFARNQALARLQGLGDSFNV -----FRIIGGILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR EDSYGLITTTRATINPGVDGTNR--IESTAVDFRS-----ALIG-----IYGVNR VDFHWKFVTHPIASDNFYYPGYAGIGT------QLQDSENELPP-EATGQPNYESYS HRLSHIGLIS------ASHVKALVYSWTHRSADRINTIEPNSITOIPLVKAFNLSSG HRISHVTFFSFQTNQAGSIANAGSVPTYVWTRRDVDLNNTITPNRITQLPLVKASAPVSG -----TIQTGIGIAGKILGTLGVPF NOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNN AAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKA YHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHL LILIRDASI FGKEMGLSSSBISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRY INQGNFSATMNRGEDLDYKTFRTVGFTT-----PFSFLDVQSTFTIGAWNFSSGNEVYI Gaps 606 Length 1157; NAPSFSAIEAAVVRNPHLLDFLEOVTIYSLLSRWS-NTOYMNWGGHKLE-Indels y Match
1997; DB 1;
Local Similarity 43.3%; Pred. No. 1.9e-96;
hes 322; Conservative 115; Mismatches 217; YLDEKRELFEIVKYAKQLHIERNM 719

g

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parasporal crystal protein - Bacillus thuringiensis (strain aizawai)
garasporal crystal protein - Bacillus thuringiensis (strain aizawai)
c;Species: Bacillus thuringiensis
c;Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004
C;Accession: Accession: Accession Accession accepted sequence of the insecticidal protein gene of Bacillus thuringiensis RATILLS Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis RATILLS Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis RATILLS PASSIS ACCESSION: AZCESSION: AZC
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                                                                                                                                                                                                                                                                                                                                                         Length 1155;
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39.2%; Score 1474; DB 2; Length 1
Best Local Similarity 44.4%; Pred. No. 3.5e-95;
Matches 315; Conservative 113; Mismatches 227; Indels
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                                                   RESULT 8
833655
parasporal crystal protein crylGal - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: 832645
R;Lambert, B.
S;Manited to the EMBL Data Library, April 1993
A;Reference number: 632645
A;Accession: 832645
A;Accession: 832645
A;Accession: United cLAM>
A;Reference: United cLAM>
A;Residues: 1-1166 <LAM>
A;Residues: 1-1166 <LAM>
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                    39.4%; Score 1482.5; DB 2; Length:
llarity 46.1%; Pred. No. 8.9e.96;
Conservative 101; Mismatches 204; Indels
  732
YGHDKKMLLEAVRAAKRLSRERNL
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 325, Conserva
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A Accession: A00025
A Molecule type: mRNA
A Residues: 1-115 KONA
A) Residues: 1-115 KONA
A) Residues: 1-115 KONA
A) Cross-references: UNIPROT: P06578
A) Experimental source: subsp. kurstaki
R) Gelser, M. 1, Schweltzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A) Title: The hypervariable region in the genes coding for entomopathogenic crystal protes;
A) Accession: A91560
A) Molecule type: DNA
A) Reference number: A91560, MUID: 87163505; PMID: 3557124
A) Ross-references: GB: M5271; NID: 9143123; PIDN: AAA22561.1; PID: 9143124
A) Experimental source: subsp. kurstaki
B) Wabiko, H.; Raymond, K.C.; Bulla Jr., b.A.
DNA 5, 305-314, 1986
A) Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal)
A) Reference number: A90955; WUID: 86300092; PMID: 3743328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1155 <CHA>
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
B;Hoffe, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckt
Eur. J. Blochem. 161, 273-280, 1986
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A;Reference number: A26461; MUID:87054026; PMID:3023091
                               parasporal crystal protein cry1Ab3 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot
                                                                               C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A90025; A91560; A90555; A26461; A24172; A29043; JD0002
C;Accession: A90025; Munitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: A26461
A,Molecule type: DNA
A,Residues: 1-730, 'L',732-784,'R',786-1155 <HOF>
A,Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
C,Cromental source: strain berliner 1715
C,Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: A90955
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-1155 < WAB>
A;Coss-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720
A;Experimental source: subsp. berliner
A;Experimental source: subsp. berliner
B;Chak, K.F.; Jen, J.C.
submitted to the EMBL Data Library, October 1990
A;Description: Complete nucleotide sequence and expression in Escherichia
A;Reference number: S14555
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Pred, No. 1.1e-94;
2; Mismatches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Gene: cry-1-2; bt2
;Superfamily: parasporal crystal protein
;Reywords: delta-endotoxin
;Reywords: delta-toxic peptide #status predicted
;82-300,Region: toxic #status predicted
;300-586/Region: insecticidal #status predicted
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Best Local Similarity 44.5%; Pre
Matches 316; Conservative 112;
                                                                                                                                                                                                                                    A;Reference number: A90025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
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parasporal crystal protein crylFa3 - Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accesion: 832649
R.Lambert, B.
R.Lambert, B.
A.Accession: 832645
A.Accession: 832645
A.Accession: 832649
A.Accession: 832649
A.Accession: 832649
A.Accession: 832649
A.Accession: 832640
A.Accession: 832640
A.Accession: 832640
C.Sepiente: 1-174 *LAM
A.Residues: 1-174 *LAM
A.Residues: 1-174 *LAM
C.Sos. Teferences: UNINECT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g2956
C.Superfamily: parasporal crystal protein
C.Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLV-------SSRNTAGNPI 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NIQNQCVPYNCLSNPEVEILSEERSTGRLPLDISLSLTRFLLSEFVPGVGVAFGLFDLIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 WPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAVKAHNLHSGSTVVRGPGFTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 NINHE----DCLKMSEYENVEPFVSASTIQTGIGIA-GKILGTLGVPFAGQVASLYSFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GELWPKGKNOWEI FMEHVEEI INOKI STYARNKALTDIKGLGDALAVYHDSLESWVGNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLEFRTIGGTLNISTQGSTNTSINPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 NFPIYGIFNPGGAIWIADEDPRPFYRT-----LSDPV------FVRGGFGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNFYYPGYAGIGTQLQ-------DSENELPPEATGQPNYESYSHRLSHI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GLISASHV-KALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGG
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.1%; Score 1471; DB 2;
Best Local Similarity 44.8%; Pred. No. 5.8e-95;
Matches 325; Conservative 103; Mismatches 202;
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13; FILGELWPKGKNOWEIFMEHVEBIINOKISTYARNKALIDLKGLGDALAVYHDSLESWVG 147 148 NRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFG 207 62 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPFAGQVASLYS 87 4 NPNINECIPYNCLSNPEVEVLGGERİETGYTPIDISLELÇELSEF-VPGAĞFVLGLVD Gaps 26; 63  $\delta$ 

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RESULT 13
A2798
parasporal crystal protein - Bacillus thuringiensis
c;Species: Bacillus thuringiensis
C;Date: 23-Aug-1997 #sequence_revision 23-Aug-1997 #text_change 09-Jul-2004
C;Accession: A22798 #sequence coding for the insecticidal fragment of the Bacillus thuring A7Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuring A,Reference number: A22798 MUD:85232070; PMID:2989108
A,Reference number: A22798
A,Reference number: A22798
A,Residues: 1-934 <kMI>
A,Gross-references: UNIPROT:0985V8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
C;Comment: The authors translated the codon ACA for residue 264 as Ser.
C;Reywords: delta-endotoxin
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                                                                                                           286 GIEGS-IRSPHIMDILNSITIYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 PFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQXAVNELFTSSNQ
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                      KEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLM
                                                324 AIEAAVVRNPHILIDFLEQVTIYSLLSR----WSNTQYMMM---WGGHKLEFRTIGGTLNI
                                                                                                                                                                                                                                                                                                                              345 APQORIVAQLGQGVYRTLSSTLYRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN
                                                                                                                                                                                                                                                                                                                                                                                           FYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 NITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATWSSGSNLQSGSFRTVGFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         634 IGLKTDVTDYHIDQVSNLVECLSDEFCLDEKKELSEKVKHAKRLSDERNL
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38.7%; Score 1454.5; DB 2;
Best Local Similarity 43.5%; Pred. No. 5.8e-94;
Matches 310; Conservative 119; Mismatches 222;
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DPINPALREEMRIQENDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG
                                                                                                                                                                                                        ----LENFDGSFRGSAQ
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                                                                                                                                                            VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S
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                                                                                                              QRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGFDSRDWIRYNQFRRELTLT
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Best Local Similarity 44.5%; Pred. No. 1.1e-94;
Matches 316; Conservative 112; Mismatches 226; Indels
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AyTtle: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal A;Rtle: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal A;Reference number: S02134; MUID:89083518; PMID:3205732
A;Reference number: S02134
A;Scatus: translation not shown
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-1155 cHAI>
A;Cross-references uviPROCT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278
A;Experimental source: strain aizawai IC1
R;Haider, M.Z.; Ellar, D.J.
A;Mol: Biol. 208, 183-194, 1989
A;Mol: Biol. 208, 183-194, 1989
A;Accession: S04994; MUID:89362455; PMID:2769751
A;Accession: S04994
A;Residues: 420-449, A', 451-724 cHAW>
A;Residues: 420-449, A', 451-724 cHAW>
A;Residues: 420-449, A', 451-724 cHAW>
A;Residues: 220-449, A', 451-724 cHAW>
A;Residues: 220-249, A', 16115
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180 QRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWYRYNQFRRELTLT 239
                                                                                                                                                                                                381
                                                                                                                                                                                                                                  286 RIEQNIRQPHLMDILNSITIYTDVHRG----FNYWSGHQITASFVGFSGPEFAFFLFGN 340
                                                                                                                                                                                                                                                                                                        INTSINPVTLPFTSRDVYRTESL-----AGLNLFLTQPVNGVPRVDFHWKFVTHPI 432
                                                                                                                                                                                                                                                                                                                                              341 AGNAAPPULVSLIGLGIFRILSSPLYRRIILGSGPN---NQELFVLDGTEFSFASLTINL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : : | | : : | | : : | | BSIIYRQRGTV-----DSLDVIPPRAGFSHRLSHVIMLSQAAGAVYILRAP 450
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C, Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C, Superfamily: parasporal crystal protein
C, Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasporal crystal protein crylCl - Bacillus thuringiensis (strain aizawai 1 N;Alternate names: delta-endotoxin ICl; entomocidal crystal protein C;Species: Bacillus thuringiensis
A;Variety: strain aizawai ICl
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: S02134; S04994
B;Haider, M.Z.; Bllar, D.J.
Nucleic Acids Res. 16, 10927, 1988
                                                                                       268 VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGFRTVGF
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                                                                                                                    240 VLDIVALFSNYDSRRYPIRTVSQLTREIYTNPV---
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N.Alternate names: 135K insecticidal protein

N.Alternate names: 135K insecticidal protein

C.Species accillus thuringiensis

A.Title: Cloning and expression in Escherichia coli of the 135-kba insecticidal protein

A.Molecule type: DNA

A.Molecule type: DNA

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                                                                                             VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327
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Best Local Similarity 43.5%; Pred. No. 9.9e-94;
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps
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377 STOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTOPVNGVPRVDFHWKFVTHPIASDN 436 : | : : | : | | | 345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395 437 FYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489 396 LPSAVYRKSGT--VDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRPPMF 453

490 SWIHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGDILRRINTGIFGDIRV 549 

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RGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719 670

셤 ò Search completed: October 28, 2004, 18:31:50 Job time: 22.191 secs

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October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds (without alignments) 3549.224 Million cell updates/sec
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3760
1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYAKQLHIERNM 719
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| cgn2 6/prodate/2/pubpaa/VSO7 PUBCOMB.pep:*
| cgn2 6/prodate/2/pubpaa/PSO6 NEW PUB.pep:*
| cgn2 6/prodate/2/pubpaa/VSO6 NEW PUB.pep:*
| cgn2 6/prodate/2/pubpaa/VSO8 NEW PUB.pep:*
| cgn2 6/prodate/2/pubpaa/VSO8 PUBCOMB.pep:*
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| cgn2 6/prodate/2/pubpaa/VSIOD_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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	Description	Sequence 10, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 7, Appli	Sequence 42, Appl	Sequence 10, Appl	Sequence 7, Appli	Sequence 63, Appl	Sequence 23, Appl	Sequence 38, Appl		Sequence 25, Appl	Sequence 1, Appli
000000000000000000000000000000000000000	ΩI	US-10-782-020-10	US-10-782-141-8	US-10-782-096-10	US-10-782-570-7	US-10-428-961-42	US-10-809-953-10	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23	US-10-428-961-38	US-10-614-524-2	US-09-826-660-25	US-10-089-678-1
	DB	17	17	17	11	14	16	10	14	σ	14	15	σ	14
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	% Query Match	100.0	100.0	100.0	100.0	92.5	9.09	60.3	58.2	57.8	56.3			
	Score	3760	3760	3760	3760	3476.5	2278.5	2265.5	2186.5	2171.5	2116	2116	1932.5	1722.5
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Sequence 6, Appli Sequence 11, Appl Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 72, Appli Sequence 72, Appli Sequence 28, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 17, Appli	7,7
4 US-10-428-961- 7 US-10-782-141- 10 US-10-782-150- 4 US-10-745-177- 10 US-10-414-637- 10 US-10-414-637- 10 US-10-414-637- 10 US-10-746-914- 10 US-10-746-914- 10 US-10-746-914- 10 US-10-914- 10 US-10-914-	-10-10 -10-78 -10-78
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US-10-782-020-10

US-10-782-020-10

Sequence 10, Application US/10782020

PUDLication No. US20040197916A1

GENERAL INFORMATION:

APPLICANT: Garozzi, Nadine

APPLICANT: Garozzi, Nadine

APPLICANT: Caris, Nichael G.

APPLICANT: Caris Brian

TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and

TITLE FEFERENCE: 056500/274139

CURRENT APPLICATION NUMBER: 0504-02-19

PRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FESTENCE for Windows Version 4.0

SEQ ID NO 10

LENGTH: 719
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ORGANISM: Bacillus thuringiensis
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Best Local Similarity 100.
Matches 719; Conservative
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100.0%; Score 3760; DB 17; Length 'Best Local Similarity 100.0%; Pred. No. 2.7e-309;
Matches 719; Conservative 0; Mismatches 0; Indels
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Publication No. US20040197917A1
GENERAL INFORMATION:
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US-10-782-141-8
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APPLICANT: Carozzi, Nadine
APPLICANT: Carozzi, Nachael
APPLICANT: Carozzi, Nichoel
APPLICANT: Moriel
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REPERENCE: 045600/274148
CURRENT APPLICATION NUMBER: 00/402-19
PRIOR PPLICATION NUMBER: 60/448,633
PRIOR FILING DATE: 2003-02-03
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
EENGTH: 719
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1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI

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APPLICANT: Buum, James A.
APPLICANT: Buum, James A.
APPLICANT: Chu, Chih.Rei
APPLICANT: Chu, Chih.Rei
APPLICANT: Chu, William P.
APPLICANT: Glimer, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Soloria Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
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                                                                                                                                                1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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                                                                        719;
                                                                          Length
                                                                                                             Indels
                                                                      100.0%; Score 3760; DB 17;
100.0%; Pred. No. 2.7e-309;
ive 0; Mismatches 0;
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; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7
                                                                                                             Conservative
                                                                      Query Match
Best Local Similarity
Matches 719; Conserv
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| Sequence 7, Application US/10782570
| Publication No. US20040210965A1
| GENERAL INFORMATION:
| APPLICANT: Carczi, Nadine
| APPLICANT: Hargiss, Tracy
| APPLICANT: Carcis, Michael G.
| APPLICANT: Carcis, Brian
| TITLE OF INVENTION: ARMI-007, A Delta-Endotoxin Gene and
| TITLE OF INVENTION: Methods for Its Use
| TITLE OF INVENTION: Methods for 128 Use
| FILE REFERENCE: 045600/274144
| CURRENT FILING DATE: 2004-02-19
| PRIOR PAPLICATION NUMBER: 05/448,812
| PRIOR PLICATION NUMBER: 60/448,812
| PRIOR PLICATION NUMBER: 60/448,812
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 7
| LENGTH: 719
                     0; Indels
 Pred. No. 2.7e-309; Mismatches 0;
Local Similarity 100.0%; Punes 719; Conservative 0;
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APPLICANT: Botterman, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henn,
TITLE OF INVENTION: CRYSTAL PROTEINS
FILE REFERENCE: 02156-078
CURRENT APPLICATION NUMBER: US/09/661,016
PRIOR PILING DATE: 2004-03-26
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 1200-09-13
PRIOR PELICATION NUMBER: GE 89401499.2
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
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Best Local Similarity 62.7%; Pred. No. 2.1e-183;
Matches 449; Conservative 80; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Bacillus thuringiensis
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   Van Mellaert, Hern
Botterman, Johan
Van Rie, Jeroen
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LENGTH: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 QTGIGIAGKILGNLGVPFAGQVASLYSFILGELWPKGKSQWEIFMEHVEELINQKISTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSBNELPPBATGQPNYESYSHRLSHIGLIS
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                                                                                                                                                                                                                                                                                                                                                                                                                         RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GTVHPHPSFTSTTWYNNNAPSFSTIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 GGHKLEFRTIGGTLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                  1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                          any naturally
                                                                                                                                                                                                                                Query Match
92.5%; Score 3476.5; DB 14; Length 710;
Best Local Similarity 92.5%; Pred. No. 2.8e-285;
Matches 665; Conservative 15; Mismatches 30; Indels 9;
                                                                                                                                                                                          for
                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (2007..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SLENGTH: 710
                                                                                                                            ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                            ; OTHER INFORM
US-10-428-961-42
                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                               TYPE: PRT
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25; Gaps

Length 1228;

70 61 130

190

250 241

181

359

416

543 535 663

FISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719

664

US-10-809-953-10
. Sequence 10, Application US/10809953
. Publication No. US20040181825A1
. GENERAL INFORMATION:

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656 FINTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

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                                                                                                                                                                                                                                         SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
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64.3%; Pred. No. 2.6e-182;
ive 78; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Innear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: US-09-988-462-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                             Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
                             Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1207 amino acids
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                                                                                                                                                                                                                                 Karen L
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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Best Local Similarity 64.3*
Matches 442; Conservative
                                                                                                                                                                                                                                                                               SEQUENCES:
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INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                              NUMBER OF
                                                                                                                                                                                                                                             TITLE OF
                    US-09-988-462-7
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Sequence 63, Application US/10428961

Sequence 63, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Depidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polymucleotides, Compositions, and Methods of Use (Amended)

FILE REPERENCE: MECO201-1

CURRENT APPLICATION NUMBER: 09/661,322

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR APPLICATION NUMBER: 60/61,322

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER: OF SEQ ID NOS: 63

SEQ ID NOS: 63

SEQ ID NOS: 63

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                                        160 SQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIST
                                                                                                                                                                                                                                                                                                     TOMYPIKTTAQLTREVYTDA1GTVHPHPSFTSTTWYNNNAPSFSA1EAAVVRNPHLLDFL
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                                                                                                                                                  FYNROVERAGDYSDHCVKWYSTGLINNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYD
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Best Local Similarity 59.2%; Pred. No. 1.3e-175;
Matches 423; Conservative 105; Mismatches 173; Indels
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; ORGANISM: Bacillus thuringiensis
US-10-428-961-63
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us-10-019-823b-55.rapb

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FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
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; Sequence 38, Application US/10428961
Sequence 18, Application US/10428961
; GENERAL INFORMATION:
                                    US-09-826-660-23
                                                                                                  Best Local Sim
Matches 421;
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Patent No. US20010026940A1

GENERAL INFORMATION.

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Narva, Kenneth B.

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

FILE REFERENCE: MA.714AC2D1

CURRENT APPLICATION NUMBER: 05/09/826,660

CURRENT FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-23

PRIOR PLICATION NUMBER: 60/065,215

PRIOR PLICATION NUMBER: 60/065,415

PRIOR PLICATION NUMBER: 60/076,445

PRIOR FILING DATE: 1999-03-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 23

LENGTH: 1186

TYPE: PRT

CURRENT FILIS CARDENT FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE PRESENCE FOR THE
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APPLICANT: Bunn, James A.
APPLICANT: Bunn, James A.
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, William P.
APPLICANT: Glimer, Mark J.
APPLICANT: Rupar, 
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h Similarity 59.0%; Score 2171.5; DB 9; Length 1186; Similarity 59.0%; Pred. No. 2.4e-174; 21; Conservative 108; Mismatches 172; Indels 13;
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APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Van Rie, Jeroen
TILLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
FILE REFERENCE: NEWETSUS2
CURRENT APPLICATION NUMBER: US/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR PLING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/173397
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1228
                                                                                                                                                                       TYPE: PRT ORGANISM: Bacillus thuringiensis
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                                                                                                                                 ; Score 2116; DB 14;
; Pred. No. 1.3e-169;
98; Mismatches 181;
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION WUMBER: 60/153,995
RUGHER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 1228
                                                                                            ) ORGANISM: Bacillus thuringiensis
US-10-428-961-38
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544 MGLNFNNTSLQRYRVRVRYRAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAE
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     Length
                                                       Indels
56.3%; Score 2116; DB 15;
59.5%; Pred. No. 1.3e-169;
ive 98; Mismatches 181;
                                                    424; Conservative
Query Match
Best Local Similarity
Matches 424; Conserv
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RESULT 12 US-09-826-660-25

Sequence 2, Application US/10614524; Publication No. US20040016020A1; GENERAL INFORMATION:

RESULT 11 US-10-614-524-2

APPLICANT: Arnaut, Greta APPLICANT: Boets, Annemie APPLICANT: Damme, Nicole APPLICANT: Mathieu, Eva

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                                                      | JOHNSTAN INTERNATION | JOHNSTAN INTERNATION | JOHNSTAN INTERNATION | JOHNSTAN INTERNATION | JOHNSTAN STERMAN | STERMAN | STERMAN | STERMAN | STERMAN | STERMAN | STERMEN | JOHNSTAN | JOH
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence PATURE: PEATURE: PEATURE: OTHER INFORMATION: Toxin encoded by synthetic B.t. US-09-826-660-25
Sequence 25, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
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APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOXIOUS ORCANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: NOXIOUS ORCANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: NOXIOUS ORCANISM-CONTROLLING AGENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: PZ 2000-236140
PRIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEC ID NOS: 3
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSFISTFYNRQVERAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANYYAQ-VYGVPYASF-----TLLDKN----TGSGSVGGFTYSKPHTTMQVCTQNYNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NELPPEATGOPNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADRINTIEPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 YSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 -RWSNTQYMNWWGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESL-AGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLKNQDKHQ---SFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYE----NV
                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 1722.5; DB 14; Length 1167;
47.9%; Pred. No. 2.6e-136;
Live 126; Mismatches 218; Indels 49; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 NLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIG
Sequence 1, Application US/10089678 Publication No. US20030017967A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                             45.8%; Sc.
Best Local Similarity 47.9%; Pr.
Matches 361; Conservative 126;
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590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEVIIDRFEFIPVTAT 640
                                                                         538 -RINIGTF---GDIRVNIN-PPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMN 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 VQKLPSFAVSGEEVPLLPIYAQAANLHILLIRDASIFGKEWGLSSSEISTFYNRQVERAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 DYSDHCVKWYSTGLNNLRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTA 289
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                                                                                                                                                           593 RGEDLDYKTFRTVGFTTPFSFLDVQSTFT-----IGAMNFSSGNEVYIDRIEFVPVEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 VEPFVSASTIQIGIAGKILGTLGVPFAGQVASLYSFILGELWP-KGKNQWEIFMEHVE
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44.4%; Score 1670.5; DB 17; Length
Best Local Similarity 49.1%; Pred. No. 6.4e-132;
Matches 371; Conservative 98; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hargiss, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENTH: 1157
TYPE: PAT
ORGANISM: Bacillus thuringiensis
US-10-782-141-16
                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 16, Application US/10782141; Publication No. US20040197917A1
GENERAL INFORMATION: APPLICANT: CAROZZI, Nadine
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641 FEVEYDLERAQK 652
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chlh.Rei
APPLICANT: Chu, Chlh.Rei
APPLICANT: Chu, Chlh.Rei
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
TITLE OF INVENTION: Deploopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Deploopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Deploopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Deploopteran-Active Bacillus thuringiensis Of Use (Amended)
TITLE OF INVENTION: Deploopteran-Active Bacillus thuringiensis Of Use (Amended)
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2000-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 64
NFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVS 685
                           ILGTIGVPFAGQVASLYSFILGELWPKGKNOWEIFWEHVEBIINQKISTYARNKALTDLK 129
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                                                                                    NLVESLSDEFYLDEKRELFEIVKYAKOLHIERNM 719
                                                                                                           Sequence 6, Application US/10428961
Publication No. US20030237111A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bacillus thuringiensis
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Search completed: October 28, 2004, 18:40:56 Job time : 68:6795 secs

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October 28, 2004, 17:52:12 ; Search time 98.2996 Seconds (without alignments) 4202.652 Million cell updates/sec
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3749
1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYAKQLHIERNM 718
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                  1825181 seqs, 575374646 residues
                                                                                OM protein - protein search, using sw model
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database :

	Description	Q45752 bacillus th	Q6x181 bacillus th	Aap86782 bacillus	Q93nj5 bacillus th	085796 bacillus th	Cac85964 bacillus	Q8ky61 bacillus th	Q9f0p8 bacillus th	Q45709 bacillus th	Q9xdl1 bacillus th	087404 bacillus th	Q45739 bacillus th	Q45774 bacillus th	Q93t75 bacillus th	P05517 bacillus th	Q93nm5 bacillus th	Q6pyw8 bacillus th	Aas93797 bacillus	O85805 bacillus th	Q8kny2 bacillus th	Q9zaz5 bacillus th	Q45715 bacillus th	Q45740 bacillus th	Q45704 bacillus th	Q8kz17 bacillus th	Q45733 bacillus th	Q45705 bacillus th	Q45746 bacillus th	O66377 bacillus th	Q45738 bacillus th	Q45749 bacillus th
SUMMARIES	ID	C1IA BACTK	Q6X1 <u>8</u> 1	AAF86782	O93NJS	085796	CAC85964	Q8KY61	Q9F0P8	C1IB_BACTE	C1ID_BACTU	Clic_Bactu	C1BB_BACTU	C1BC_BACTM	Q93T75	C1BA BACTK	Q93NM5	Q6PYW8	AAS93797	CIBE_BACTU	QBKNY2	C1BD_BACTZ	C1KA BACTM	Q45740	C8AA_BACUK	Q8KZL7	C9CA_BACTO	C8BA_BACUK	1 C1GA_BACTU	C1FB_BACTM	C1JA_BACTU	Q457 <u>4</u> 9
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## ALIGNMENTS

RESULT	17 1 BACTY
5	CITE BACHK STANDARD BRT: 719 AA
A	0457 <u>5</u> 2; P71092; 045750; 045751; 045756;
TO	30-MAY-2000 (Rel. 39, Created)
ΠŪ	30-MAY-2000 (Rel. 39, Last sequence update)
티	05-JUL-2004 (Rel. 44, Last annotation update)
E I	crystal protein crylla (Insecticidal delta-endot
DE	rystaline entomocidal protoxin) (
g S	Name=crylla; Synonyms=cryll(a), cryV, cryVl, CGCryV;
SO	
3 5	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
X S	NCB_TaxID=29339;
3 5	יייי עריייייייייייייייייייייייייייייייי
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י ני	SIKAIN=DSIK/32;
ž ;	MEDLINE=942/8000/ PUDMed=851/58%
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X 0	
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Z.	Appl Environ Microbiol 59:1683-1687 (1993)
RN	
g G	SECUENCE PROM N.A.
EC.	STRAIN=UHCC4835;
KX.	MEDLINE=92269582; PubMed=1588820;
RA	Tailor R., Tippett J., Gibb G., Pells S., Pike D., Jordan L., Elv S.,
RT	"Identification and characterization of a novel Bacillus thuringiensis
RT	intomocidal to coleopte
RL	Mol. Microbiol. 6:1211-1217(1992).
RN	[3]
RP	SEQUENCE FROM N.A.
R	STRAIN=HD-1;
RX	MEDLINE=95314293: PubMed=7793960;
RA	Shin BS., Park SH., Choi SK., Koo B.T., Lee S.T., Kim J.I.;
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus
R	thuringiensis and cloning of cryV-type genes from Bacillus
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RŢ	entomocidus.";
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).
Z	[4]
ያ ያ	SEQUENCE FROM N.A.
2 i	STRAIN=ABB8;
ž	
KA :	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
RA:	
R.T.	"Cloning of a cryv-type insecticidal protein gene from Bacillus
4 6	triutingrenss: the cryv-encoded process as expressed early in
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                                                                                                                                                                                                                                                                                                                          TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
                                                                                                                                                                                                                                                                                                                                                                  TGINNIRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                                                                                1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
                                                                                         VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                         TEXIVGETIPFSLLDVQSTFIIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis.
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03945; Endotoxin_N; 1.
SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;
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Pred. No. 1.2e-251;
); Mismatches 3;
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Interpro; IPR001178; Endotoxin.
Interpro; IPR005639; endotoxin.C.
Interpro; IPR005639; endotoxin.N.
Interpro; IPR008639; endotoxin.N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PP03944; Endotoxin.C; 1.
Pfam; PP03945; Endotoxin.M; 1.
Pfam; PP03945; Endotoxin.M; 1.
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Best Local Similarity 99.4*
Matches 715; Conservative
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05-JUL-2004
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-> Y (in strain JHCC4835 and strain HD-
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                                                                                               FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species. Active on Plutella xylostella and Bombyx mori. DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
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                                                                                                                                                                                                                                                   the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the
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A -> V (in strain AB88).
KQ -> NE (in strain HD-1 and strain KQ -> NE (in strain HD-1).
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                                           "Isolation, cloning and expression of cryV gene."; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001178; Endotoxin.
Interpro; IPR005639; endotoxin.C.
Interpro; IPR005639; endotoxin.N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PP03944; Endotoxin_C; 1.
Pfam; PP03555; Endotoxin_M; 1.
Pfam; PP03345; Endotoxin_N; 1.
                     Bhatnagar R.K.;
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EMBL, X62821, CAA44633.1, --
EMBL, L36338, AAC36999.1, --
EMBL, L49391, AAC00968.1, --
EMBL, X08220, CAA70124.1, --
EMBL, X39815, I33815.
PIR, S25383, S35383.
HSSP, P02965, ICIY
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719 AA; 81216 MW;
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Matches 715; Conservative
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                     Selvapandiyan A.,
                                                                                                                                                                                                                                                                                                              terminus.
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VARIANT
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SEQUENCE
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                                  241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                     301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEGVTIYSLLSRWSNTQYMMW
                                                                                                                                                                                                                                    GCHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
                                                                                                                                                                                                                                                                    421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
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Song F. Zhang J., Gu A., Huang D., Li G.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR373207; AAK66742.1; -.
HSSP, P02965; ICTY.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0006552; P:pdefense response; IEA.
GO; GO:000405; P:pathogenesis; IEA.
InterPro; IPR00178; Endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR006539; endotoxin.
InterPro; IPR006539; endotoxin.
InterPro; IPR006539; endotoxin.
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Last sequence update)
Last annotation update)
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Pred. No. 2.6e-251;
0; Mismatches 4;
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Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae;
NCBI_TaxID=1428;
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Pfam; PF0355; Endotoxin_M; I.
Pfam; PF03945; Endotoxin_M; I.
SEQUENCE 719 AA; 81225 MW;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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            GTVHPHPSFTSTTWYNNNAPSFSALEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW 360
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                                                                                                                                                                              GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVXRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                  GGHKLEFRIIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
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STRAIN-T01 328;
Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
"Complete sequence of cryll gene of isolate T01 328 from luturingiensis from Cubatao (SP - Brazil) soil.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY262167; AAP86782.1; --.
SEQUENCE 719 AA, 81216 MW; 3627E5A6C25DAFF5 CRC64;
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=1428;
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99.3%; Score 3722.5; DB 2
Best Local Similarity 99.4%; Pred. No. 1.2e-251;
Matches 715; Conservative 0; Mismatches 3;
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                                    pred. No. 3.1e-251;
0; Mismatches 4: 7-7
              81230 MW; 42746D478359BBA7 CRC64;
                                                        Query Match
Best Local Similarity 99.3%; Pred. No. 3.1e
Matches 714; Conservative 0; Mismatches
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SEQUENCE FROM N.A.
STRAIN=BNS3;
Tounsi S.; Zouari N., Jaoua S.;
                      719 AA;
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                                                                                                                                                                   TGLNNLRGTNAESWYRYNQPRRDMTLMVLDLVALPPSYDTQMYPIKTTAQLTREVYTDAI
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STRAIN-6101;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AP076939; AAC26910.1; -.
HSSP; PO2965; JCIY.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0009405; P:defense response; IEA.
RG; GO:0006405; P:pathogenesis; IEA.
RG; GO:0006405; P:pathogenesis; IEA.
RICEPTO: IPRO0178; Endotoxin.C.
NR InterPro: IPRO08638; endotoxin.C.
NR InterPro: IPRO08639; endotoxin.C.
NR InterPro: IPRO08639; endotoxin.C.
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DR Féan; PP03945; Endotoxin.C; I.
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Plasmid large plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-NOV-1998 (TrEMBLrel. 08, C;
01-NOV-1998 (TrEMBLrel. 08, L;
01-MAR-2004 (TrEMBLrel. 26, L;
Insecticidal protein.
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EMBL; AF278797; AAM73516.1; --
R PIR; B42459; B42459.
R PIR; B42459; B42459.
R GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0006952; P:defense response; IEA.
R GO; GO:00009402; P:redense response; IEA.
R InterPro; IPR001178; Endotoxin.
R InterPro; IPR005639; endotoxin.
R InterPro; IPR008979; Gal. bind. Tike.
R InterPro; IPR008979; Gal. bind. Tike.
R InterPro; IPR008979; Gal. bind. Tike.
R Pfam; PF03944; Endotoxin. C: 1.
R Pfam; PF03945; Endotoxin. M; 1.
R Pfam; PF03955; Endotoxin. M; 1.
R Pfam; PF03955; Endotoxin. M; 1.
S SEQUENCE 719 AA; 809964 MW; 84F1287246264473 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                95.7%; Score 3587.5; DB 2; Length
95.7%; Pred. No. 3.3e-242;
iive 12; Mismatches 18; Indels
         EMBL/GenBank/DDBJ databases
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Best Local Similarity 95.7
Matches 688; Conservative
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      crylla-type gene
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                                                                                                                                719;
                                                                                                                                Length
                                                                                                                                                                         4; Indels
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
"Cloning and study of the expression of a novel crylla-
Bacillus thuringiensis subsp. kurstaki.";
J. Appl. Microbiol. 95:32-28(2003).
EMBL, AJ315121; CAGS5964.1; -
SEQUENCE 719 AA; 81203 MW; 8676ESA6C25DAFE8 CRC64;
                                                                                                                            Query Match
99.1%; Score 3714.5; DB 2;
Best Local Similarity 99.2%; Pred. No. 4.2e-251;
Matches 713; Conservative 1; Mismatches 4;
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(TrEMBLrel. 22, I
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Q8KY61;
01-OCT-2002 (TFEMBLrel. 2:
01-CCT-2002 (TFEMBLrel. 2:
01-MAR-2004 (TFEMBLrel. 2:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                              TEXTVGFTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEXDFEKAQEKV
                                                                                                                         entomocidus.";
Appl. Environ. Microbiol. 61:2402-2407(1995).
-!-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.
Active on Plutella xylostella but not on Bombyx mori.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part c
                                                                                                                                                                                                    TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
50-JUL-2004 (Rel. 44, Last annotation update)
65-JUL-2004 (Rel. 44, Last annotation update)
65-JUL-2004 (Rel. 44) Last annotation update)
65-JUL-2004 (Rel. 45) Rel. 67-May annotation update)
67-JUL-2004 (Rel. 45) Rel. 67-May annotation update)
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Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.,
Distribution of cryV-type insecticidal protein genes in Bacillus
thuringiensis and cloning of cryV-type genes from Bacillus
thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the
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Best Local Similarity 92.4%
Matches 664; Conservative
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SEQUENCE 719 AA;
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In Appl. Environ. Microbiol. 69:5207-5211(2003).

R HSSP; PO2265; LICIY.

R GO; GO:0009615; F:receptor binding; IEA.

GO; GO:0009605; P:pathogenesis; IEA.

R GO; GO:0009405; P:pathogenesis; IEA.

R GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPRO05639; endotoxin.

R InterPro; IPRO05639; endotoxin.

R Pfam; PF00354; Endotoxin. M; 1.

R Pfam; PF00355; Endotoxin. M; 1.
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                                                                                                                                                                                    Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  719 AA; 81024 MW; 7E17481922C435E6 CRC64;
Created)
Last sequence update)
Last annotation update)
     (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 669; Conservative
                                                                                                                                  Bacillus thuringiensis
Plasmid pBTC19.
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                               NCBI_TaxID=1428;
                              01-MAR-2001
01-MAR-2004
                                                                                                            Name=crylI;
                                                                                                                                                                                      Bacteria;
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             segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
                                                                                                                                                                                                                                                                                           Pfam; PP03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF00555; Endotoxin_N; 1.
Sporulation; Toxin.
SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
                                             SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                         89.6%; Score 3359.5; DB
89.3%; Pred. No. 3e-226;
ive 35; Mismatches 4
                                                                                                                                                                                               EMBL; AF047579; AAD44366.1; -.
HSSP; P02965; 1CIX.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008979; Gal_bind_like.
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Best Local Similarity 89.39
the spore coat.
MISCELLANEOUS: Toxic
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                                                QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFWEHVEEIINQKILTYA
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                                                                                                                                                                                    EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNROVERTRDYSDHCIKWYN
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MKLKNPDKHQSLSSNAKVDKI ATDSLKNETDI ELKNMNNEDYLRMSEHESIDPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TALFISINPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFELVKYAKQIHIERNM
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-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae. Active on Plutella xylostella and on Bombyx mori xylostella and on Bombyx mori The Orbit Elevente is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TALFISINPRGLKIDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
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Da crystal protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BR30;
MEDLINE=20374042; PubMed=10919402;
Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
"Cloning of a new Bacillus thuringiensis cryll-type crystal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
Pesticidal crystal protein crylld (Insecticidal del Cryll(d)) (Crystaline entomocidal protexin) (81 kba Name-crylld; Synonyms=cryll(d), NRcryV;
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                                                                                                           361 GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDFYRTESWAGLNLFLTQPVNGVPR
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30-MAY-2000 (Rel. 39, Last sequence update)
05-MOL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBb (Insecticidal delta-endotoxin CrylB(b)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                      GTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW
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STRAIN=NRE B-21110 / EGS847;
STRAIN=NRE B-21110 / EGS847;

"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins toxic to legidopteran insects.";

Patent number US5322687, 21-JUN-1994.

-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithellal cells of many lepidopteran larvae.

-i- FUNCTION: ATRAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
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HSSP, P02965; 1CIY.
InterPro; IPR001178; Endotoxin.
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  TALFISINPRGLKIDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
                          TAMFISTNIERELKTINVTDCHIDQVSNIVESLSDEFYLDEKRELFEIVKYAKQINIERNM 719
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                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylic (Insecticidal delta-endotoxin
Cryli(c)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C18 / ESYPE;
SOBRAIN Y.A., MadKour M.A., Bulla L.A. Jr.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- EVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminus. SimilaRITY: Belongs to the delta endotoxin family.
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Plasmid; Sporulation; Toxin.
SEQUENCE 719 A4, 91210 MW; 8370B3F06B905DFF CRC64;
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                                                                                                                                                              719 AA
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IPR005638; endotoxin_C.
IPR005639; endotoxin_N.
IPR008979; Gal_bind_like.
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Pfam; PP00555; Endotoxin_M; 1.
Pfam; PP03945; Endotoxin_N; 1.
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Matches 644; Conservative
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                   Name=cryllc; Synonyms=c
Bacillus thuringiensis
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Matches 467,
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
CrylB(c)) (Crystaline encomocidal protoxin) (140 kDa crystal protein)
Name=crylBc, Synonyms=crylB(c), crylBc,
Bacillus thuringiensis (subsp. morrison)).
                                                                                                       Gaps
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                                                                                     Length 1229;
                                                                                    Score 2415; DB 1; Length 1; Pred. No. 8.2e-160; 91; Mismatches 141; Indels
                                                                   A4C949DB675C3269 CRC64;
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InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR005639; endotoxin_N.
Pfam; PP03944; Endotoxin_C; 1.
Pfam; PP03555; Endotoxin_M; 1.
Spam; PP03545; Endotoxin_M; 1.
Sporularion; Toxin.
SEQUENCE 1229 AA; 139769 MW; A4C94
                                                                                    64.4%;
65.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMWGGHKLEFRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKALTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRNTAIARLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAANLHLLLLRDASI FGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STNWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYWVGHRLNFRPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVKALVYSWTHRSADRTNT1EPNS1TQ1PLVKAFNLSSGAAVVRGPGFTGGD1LRRTNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                 Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
                                                                                                                                                                                                                                                                                                                             the spore coat.
MISCELLANBOUS: Toxic segment of the protein is located in the
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                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: The crystal protein is produced dui sporulation and is accumulated both as an inclusion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.4%; Score 2415; DB 1; 165.1%; Pred. No. 8.2e-160; ive 91; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR00879; Gal_bind_like.
Pfam; PF03944; Endotoxin_C; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF0555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
Spornlation; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001178; Endotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z4642; CAA86568.1; -. HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 65.1
les 467, Conservative
   Firmicutes;
                                                                                        SEQUENCE FROM N.A.
                               NCBI_TaxID=1441;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPI 359
                                                                                                                                                                                                                                                                                                                                                                                                                  476 VNVPVYSWTHRSADRINTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRINTGG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE SEL.Kurstaki, STRAIN=HD-2;
MEDILINE=88203216; PubMed=3362680;
Brizzard B.L., Whiteley H.R.;
"Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis;";
Nucleic Acids Res. 16:2723-2723(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVGFTTPFSLLDVQSTFT1GAMNFSSGNEVYIDRIEFVPVEVTYEABYDFEKAQEKVTAL
                                                                                                                                                                                                          THP----IASDNFYYPGYAGIGTQLQDSENELPPEATGOPNYESYSHRLSHIGLISASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536 PGPIRVTVNGPLTORYRIGFRYASTVDFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFV
                                                                                                       FISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta-endotoxin
kDa crystal protein)
                                                                                                                                                                                                                                                                                                                                                   VXALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES B. L. entomocidus; STRAIN=HD-110; Soctaert P.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: Promoces colloidosmotic lysis by binding to the midgut epithelial cells of insects. epithelial cells of insects.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C1BA_BACTK STANDARD; PRT; 1228 AA.

(2 D0537; Q45731;
(3 D1-NOV-1998 (Rel. 33, Last sequence update)
(4 D1-VUL-2004 (Rel. 34, Last annotation update)
(5 D-VUL-2004 (Rel. 34, Last annotation update)
(6 C-VUL-2004 (Rel. 34, Last annotation update)
(7 D-VUL-2004 (Rel. 34, Last annotation update)
(8 D-VUL-2004 (Rel. 34, Last annotation update)
(8 D-VUL-2004 (Rel. 34, Last annotation update)
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(9 D-VUL-2004 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X06711; CAA29898.1; -. EMBL; X95704; CAA65003.1; -.
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CIBA_BACTK
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                                                                                                                                                                                    900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
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                                                                                                                  601
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                                                                                                                                                                                                                                                                                                                                                                                               662 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
                                                                                                                                                                                                                                                                                                                                                                                                                             TERAPVYSWTHRSADRINIIGPNRITQIPLVKALNLHSGOVTVVGGPGFTGGDILRRING
                                                                                                                                                       601 RTAGFSTPFNFLNAQSTFTLGAQSFSN-QEVYIDRVEFVPAEVTFEAEYDLERAQKAVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : ||| :| ||| || || || ||| ||| ||| || TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEBIINQKISTYARNKALTDLKG
                                                                                                                  TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
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Pred. No. 3.4e-148;
0; Mismatches 164; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mat Isa M.N.; Abdullah M.A.F., Mahadi N.M.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, AF835025; AAK51084.1; -.

RHSD, AP835025; AAK51084.1; -.

GO; GO:0005102; F:receptor binding; IEA.

GO; GO:0005952; P:defense response; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

R GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPR00178; Endoctoxin.

R InterPro; IPR005539; endoctoxin.

R InterPro; IPR005639; endoctoxin.

R InterPro; IPR005639; endoctoxin.

R Pfam; PF03944; Endotoxin.

R Pfam; PF03945; Endoctoxin.

R Pfam; PF03945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-cry1Ba2;
Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Delta-endotoxin CrylBa2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=HD-9;
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71 LGTLGVPFAGQVASLYSFILGELWPKGKNOWEIFMEHVEELINQKISTYARNKALTDLKG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 LGVLGVPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQG 121
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62.3%; Pred. No. 4e-148;
Live 80; Mismatches 164; Indels 26;
| PIR; S00873; S00873. |
| HSSP; P07130; 1DLC. |
| InterPro; 1PR001178; Endotoxin. |
| InterPro; 1PR001178; endotoxin. |
| InterPro; 1PR008979; endotoxin. |
| InterPro; IPR008979; endotoxin. |
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Best Local Similarity 62.3%;
Matches 446; Conservative
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Search completed: October 28, 2004, 18:29:48
Job time : 102.442 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 28, 2004, 18:05:43 ; Search time 19.191 Seconds (without alignments) 3604.811 Million cell updates/sec

US-10-019-823B-56 3762 1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYANELHIERNM 719 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	insecticidal prote	ysta	insecticidal prote	cryV465 protein -	parasporal crystal	10	l crysta	arasporal crysta	arasporal cryst	arasporal crysta	arasporal crysta	arasporal crysta	arasporal	arasporal crysta	arasporal crysta	arasporal crysta	arasporal crysta	arasporal crysta	arasporal crysta	arasporal crysta	arasporal crysta	arasporal	al crysta	arasporal c	arasporal crysta	arasporal crysta	arasporal crysta	arasporal cryst	arasporal crysta
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S32647	S11446	JC7140	S32689	I40589	USBSXH	A49785	A27323	S10228	139811	JH0261	S11445	S19306	USBS8I	B29838	I39870
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		31.9		31.1		30.5				26.1	24.6	.2	21.8 1	.5 18.1	.4

## ALIGNMENTS

421 UDFHWKFVTHPIASDNFYYPGYAGIGTOLODSENELPPEATGOPNYESYSHRLSHIGLIS 480 421 UDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGOPNYESYSHRLSHIGLIS 480 481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN 540	OY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDENBLPPEATGQPNYESYSHRLSHIGLIS 480
TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK TFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV	541 TGTFGDIRVNINPPFAQRYRVRIRVASTTDLQFHTSING 601 TFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIE
601 TERTVÖFTTPESFLÖVGSTFTIGANNESGANEVIINTIETEN VITAL HERAGEKV 660 661 TALFTSTNPRGLKTDVKDXHIDOVSNLVBSLESEFYLDEKRELFEIVKYANBLHIBRNM 719 661 TALFTSTNPRGLKTDVKDXHIDOVSNLVBSLSDEFYLDEKRELFEIVKYANBLHIBRNM 719 661 TALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDEFYLDEKRELFEIVKYANBLHIBRNM 719	FLDVQSTFTIGAMNFS: KTDVKDYHIDQVSNLVI               KTDVKDYHIDQVSNLVI
RESULT 2 S25383 Barasporal crystal protein crylIal - Bacillus thuringiensis N.Alternate names: delta-endotoxin; parasporal crystal protein cryV C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004 C;Accession: S25383 R;Tatallor, R; Tipperion and characterization of a novel Bacillus thuringiensis delta-end A;Accession: S25383 A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end A;Accession: S25383 A;Molecule type: DNA A;Accession: S25383 A;Molecule type: DNA A;Accession: S25383 A;Molecule type: DNA A;Accession: C;Cenetics: A;Gene: CryV C;Cenetics: A;Gene: CryV C;Superfamily: parasporal crystal protein C;Seywords: delta-endotoxin	RESULT 3 I13915 Insecticidal protein cryv - Bacillus thuringiensis C.Species: Bacillus thuringiensis C.Species: Bacillus thuringiensis C.Species: Bacillus thuringiensis C.Accession: 139815 R.Gleave, A.P.; Williams, R.; Hedges, R.J. R.Gleave, A.P.; Williams, R.; Hedges, R.J. A.Ppl. Environ. Microbiol. 59, 1683-1687, 1993 A.Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for tiensis subsp. kurstaki. A.Reference number: 139815, MUID:93298009; PMID:8517758 A.Accession: 139815 A.Accession: 139815 A.Accession: DASA A.Residues: 1-719 - RASA A.Residues: 1-719 - RASA A.Residues: 1-719 - RASA A.Genetics: C.Ye C.Genetics: C.YV C.Superfamily: parasporal crystal protein
B 2; Length 719; -251; Indels 0; Gaps 0;	Query Match Best Local Similarity 99.8%; Pred. No. 2.6e-250; Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
KVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFV 	Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSBYENVEBFVSASTI 60
61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNOWEIFWEHUEEIINQKISTYA 120 	Qy 61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA 120
121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 	Qy 121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELWFVQKLPSFAVSG 180
181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240 	Qy 181 EEVPLLPIYAQAANLHLLLLEDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  181 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240
241 TGLNNLRGTNAESWVRYNOPRRDMTLMVLDLVALFPSYDTCMYFIKTTAQLTREVYTDAI 300 241 TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTCMYFIKTTAQLTREVYTDAI 300	Qy 241 TGLNNLRGINAESWYRYNQFREDMTLWVLDLVALFPSYDTQNYPIKTTAQLTREVYTDAI 300 
301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAUVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360	OY 301 GTVHPHDSFISTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNTQYMNMW 360 
361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420 	OY 361 GGHKLEFRIIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

<i>상</i> 원	421 VDFHWKFVTHPIASDNFYYPQYAGIGTQLQDSENELPPEATGOPNYESYSHELSHIGLIS 480	QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy -qq	481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540	QY 481 ASHVKALVYSWTHRSADRITNIIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGDILRRIN 540
ري 19	541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600	Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATWNRGEDLDYK 600 
QZ Dp	601 TERIVGETIPESFLDVQSTFIIGAMNESSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 660	Qy 601 TFRTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 660
Qy Dp	661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719	Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKBELFEIVKYANELHIERNM 719 
RESULT 4 140590 cryV465 C;Specie C;Date: C;Access R;Shin, Appl. Er A,Title. A,Title. Licencial	RESULT 4  140590 cryV465 protein - Bacillus thuringiensis cryV465 protein - Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004 C;Accession: 140590 R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I. A;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I. Appl. Environ. Microbiol. 61, 2402-2407, 1995 A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tomocidus. A;Reference number: 139814; MUID:95314293; PMID:7793960	RESULT 5 S00873 parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis NyAlternate names: parasporal crystal protein cryA NyAlternate names: parasporal crystal protein cryA C;Species: Bacillus thuringiensis subsp. thuringiensis C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: 800873 R;Brizzard, B.L.; Whiteley, H.R. Nucleic Acids Res. 16, 2723-2724, 1988 A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t A;Reference number: 800873; MUID:88203216; PMID:3362680
A, Acces A, Status A, Molecu A, Residi A, Cross C, Geneti	<pre>ision: I40590 is: preliminary; translated from GB/EMBL/DDBJ iule type: DNA iule type: DNA iule type: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672 i.cs:</pre>	A;Accession: S00873 A;Molecule type: DNA A;Rosidues: 1-1228 cBRI> A;Rosidues: 1-1228 cBRI> A;Cross-treferences: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g580945 C;Genetics: A;Gene: cryA4
A,Gene: C,Super:		A,Start codon: TTG C,Superfamily: parasporal crystal protein C,Keywords: delta-endotoxin
Query Best Match	Query Match 93.1%; Score 3503; DB 2; Length 719; Best Local Similarity 92.5%; Pred. No. 9.5e-234; Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;	Query Match Best Local Similarity 62.4%; Pred. No. 9.6e-148; Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;
. qq	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI 60 	
oy. Op	61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA 120 	71 LGTLGVPFAGQVASLYSFILGELMPKGKNOWEIFMEHYBEIINOKISTYARNKALTDLKG
oy Dp	121 RNKALTDLKGLGDALAVYHOSLESWYGNRNNTRARSYVKSQYIALELMFVQKLPSFAVSG 180 121 RNKALSDLRGLGDALAVYHESLESWYENRNNTRARSYVKNQYIALELMFVQKLPSFAVSG 180	QY 131 LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYA 190 
S G	BEVPLLPIYAQAANIHLLILRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS	191
상 음 당	241 TGLNNLRGINAESWYRYNQPRRDMTLMVLDLVALFESYDTOWYPIKTTAGLIREVYTDAI 300 241 TGLNNLRGINAKSWVRYNQFRKDMTLMVLDLVALFESYDTLVYPIKTTSQLTREVYTDAI 300	QY 251 AESWVRYNQFREDMILMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
S SS	301 GTVHPHPSFISTIWYNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360 301 GTVHPNQAFASTIWYNNNAPSFSAIBAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMW 360	311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNTOYMNWGGHKLEFRTI
\ \ \ \ \	361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420 	Qy 371 GGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFV 42  Db 360 GGGLNTSTHGATNTSINPVTLRPASRDVYRTESYAGVILMGIYLEPIHGVPTVRRPF 41

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C'Species: Bacillus thuringiensis
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R'Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C'Stotambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C'Status: Isolation and characterization of a novel insecticidal crystal protein gene 1 A; Reference number: A42459; MUD:91286178; PMID:2061280
A; Returns: preliminary
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A; Molecule type: DNA
A; Crose-references: UNIFROT:Q8KY61; UNIPROT:Q45740; GB:M63897
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                                                         VNVPVYSWTHRSADRTNTIGPNRITQIPMVKASBLPQGTTVVRGPGFTGGDILRRTNTGG
                                                                                         FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATWNRGEDLDYKTFR
                                                                                                                                     TVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTAL
                                                                                                                                                 FISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
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----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH
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95.3%; Pred. No. 6.7e-123;
live 8; Mismatches 10;
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Matches 362; Conservative
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39.4%; Score 1483; DB 1;
Best Local Similarity 43.1%; Pred. No. 5.7e-94;
Matches 321; Conservative 113; Mismatches 220;
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Cypecies: Bacillus thuringiensis
Cybactes: Bacillus thuringiensis
Cybacesion: S3249
Rylambert, B.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S32645
A/Reference number: S32645
A/Reference to the EMBL Data Library, April 1993
A/Reference number: S32645
A/Reference number: S32645
A/Rocession: S32649
A/Reference LDA
A/Rocession: BAA
A/Residues: 1-1174 < LAM>
A/Ross-references: UNIPROTIQ45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g295865; Reywords: delta-endotoxin
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| GGNLESGNFRTAGFSTPFSFSNAQSTFTLGTQAFSN-QEVYIDRIEFVPAEVTFEAESDL
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                                       cry1Fa3 - Bacillus thuringiensis
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                                       crystal protein
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parasporal crystal protein crylGal - Bacillus thuringiensis
C;Species Bacillus thuringiensis
C;Date: 20-Beb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S32645
A;Lambert, B.
Submitted to the EMBL Data Library, April 1993
A;Reference number: S32645
A;Accession: S32645
A;Cacesr-references
C;Access-references
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C;Access-references
C;Access-references
C;Acverder delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEDLYTRLISNIQEYSDHCARWYNQGINEIGGISR----RYLDFQRDLIISVLDIVALFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLDFLEQVTIYSLLSRWSNTQYMNWGGHKLEFRTIG-GTLN-----ISTQGSTNTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCLKMSEYE----NVEPFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPK
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCLNNPESEIFNARNSNFGLVSQVSSGL---TRFLLEAAVPEAGFALGLFDIJWGAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSE
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                                                                                                                                                                                                                                                                                                                                     39.0%; Score 1467.5; DB 2;
45.8%; Pred. No. 6.8e-93;
live 100; Mismatches 207;
 732
YGHDKKMLLEAVRAAKRLSRERNL
                                                                                                                                                                                                                                                                                                                                                    Similarity 45.8
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Best Local S
Matches 323
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NAME S. 305-314, 1986

A.Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product analy A.Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product analy A.Fitle: Bacillus thuringiensis entomocidal protoxin gene sequence analy A.Accession: A90955

A.Accession: A90955

A.Accession: A90955

A.Molecule type: DNA

A.Rocession: 1.1155 - WAB>
A.Rocession: A.Boriner and S. WAB>
A.Rocession: A.Boriner and S. WAB>
A.Rocession: A.Boriner and S. WAB>
A.Rocession: A.Boriner and S. WAB>
A.Rocession: A.Boriner and S. WAB>
A.Rocession: Complete nucleotide sequence and expression in Escherichia coli of a cry of A.Rocession suppliers and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Rocession and S. Roces
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A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
R;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckl
R;Hofte, H.; de Greve, J. 273-280, 1986
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A;Reference number: A26461; MUID:87054026; PMID:3023091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Restidues: 1-1155 <KCN>
A;Cross-references: UNIPROT:P06578
A;Experimental source: subsp. kurstaki
R;Geiser, M; Schweitzer, S.; Grimm, C.
Gene 49, 109-118, 198-6
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal protei
A;Reference number: A91560; MUID:87163505; PMID:3557124
parasporal crystal protein crylAb3 - Bacillus thuringiensis
NyAlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal
C;Specias: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A90025; A91560; A90555; S14555; A26461; A24172; A29043; JD0002
C;Accession: A90025; A91560; A91600;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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A,Residues: 1-730,'L',732-784,'R',786-1155 <HOF>
A,Cross-references: GB:X04698; NID:940254; PIDN:CAA28405.1; PID:940255
A,Experimental source: strain berliner 1715
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IGIAGKILGTLGVPFAGOVASLYS
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A;Molecule type: DNA
A;Residues: 1-1155 <GEI>
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A;Cross-reference: subsp. kurstaki
A;Experimental source: subsp. kurstaki
R;Wabiko, H; Raymond, K.C.; Bulla Jr., L.A.
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C;Keywords: delta-endotoxin
F;82-386/Product: toxic peptide #status predicted <TXP>
F;82-300(Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 38.6%; Score 1452; DB 2; al Similarity 44.2%; Pred. No. 7.8e-92; 314; Conservative 111; Mismatches 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A90025
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                       paragoral crystal protein - Bacillus thuringiensis (strain aizawai)
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004
C;Accession: A26513
R;Oeda, K.; Oshie; K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
Gene 53, 113-119, 11987
A;Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 TOGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPRVDFHWKFVTHPIASDNF 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILGELWPKGKNOWEIFMEHVEELINOKISTYARNKALTDLKGLGDALAVYHDSLESWVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPFAGQVASLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFG
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Best Local Similarity 44.1%; Pred. No. 2.6e-92;
Matches 313; Conservative 112; Mismatches 230; Indels
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148 NRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFG 207

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Darasporal crystal protein - Bacillus thuringiensis
C.Species: Bacillus thuringiensis
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C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
R.Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
J. Balotechnol. 6, 307-322, 1987
A.Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki h. A.Facesaion: 139838
A.Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki h. A.Facesaion: 139838
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A.Facesaion: 139838
A.Facesaion: 1155 ARES-
A.Cross-references: UNIPROT: PO6578; GB:M37263; NID:g142885; PIDN: AAA22420.1; PID:g142886
C.Superfamily: parasporal crystal protein
C.Superfamily: Parasporal crystal protein
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                               KEWGLSSSEISTFYNROVERAGDYSYHCVKWYSTGLNNIRGTNAESWVRYNOFRRDMTLM 267
                                                                                                                          VLDLVALEPSYDTQMYPIKTTAQLTRBVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S 323
                                                                                                                                                                               -- LENFDGSFRGSAQ 285
                                                                                                                                                                                                                                                        286 GIEGS-IRSPHIMDILNSITIYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNA 344
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                                                            396 LPSAVYRKSGT--VDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 AIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNTQYMNM---WGGHKLEFRTIGGTLNI
                                                                                                                                                                                                                                                                                                                            377 STQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDN
                                                                                                                                                                                                                                                                                                                                                                                                                          437 FYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNP
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                                                                                                                                                                                                                                                                                                                                                                      345 APOORIVAOLGOGVYRTLSSTLYRRPFNIGIN---NOOLSVLDGTEFAYG-----TSSN
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                                                                                                                                                       240 VLDIVSLFPNYDSRTYPIRTVSQLTREIYINPV---
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A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. Kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29125
B;C,Technology 5, 807-813, 1987
B;C,Technology 5, 807-813, 1987
B;C,Technology 5, 807-813, 1987
B;C,Technology 5, 807-813, 1987
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DPINDALREEMRIQENDMNSALITTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG 179
                                                                                                                                                                                              240 VLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV------LENFDGSFRGSAQ 285
                                                                                                                                                                                                                                                                                                                                                              377 STQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDN 436
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                                                                                                                                                                                                                                                                                               437 FYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489
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                                                                      KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLMNLRGINAESWVRYNQFRRDMTLM 267
                                                                                                                                                                    VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRNNTRARSVVKSQYIALELMFVQKLPSPAVSGEEVPLLPIYAQAANLHLLLLRDASIFG 207
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                                                                                                   396 LPSAVYRKSGT--VDSLDEIPPQNNNVPFRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGLKTDVKDYHIDQVSNLVBSLSDEFYLDEKRELFELVKYANELHIERNM 719
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OY 268 VLDLVALFPSYDTQMYPIXTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327		398 PSTIYRQRGTVSLDVIPPQDNSVPPRAGFSHRLSHVTWLSQAAGAVYLRAP 488 VYSWTHRSADRINTIEPNSITQIPLVKAPNLSSGAAVVRGPGFTGGDILRRINTGTFGDI :	Db 511 RVNITAPLSQRYRVRIRYASTINLQFHISIDGRPINQGNFSAIMSSGSNLQSGSFKIVGF 570  Qy 608 TIPFSPIDVQSTFIIGAMNFSSGNEVYIDRIBFVPVBVTYEAEYDFERAQEKVTALFTST 667  Db 571 TIPFNFSNGSSVPTLSAHVFNSGNEVYIDRIBFVPRATFFABEYDLERAQKAVNBLFTSS 630  Qy 668 NPRGLKTDVKDYHIDQVSNLVESLSDBFYLDERREFEBIVKYANBLHIERNM 719  C3. NGTGKTDVKDYHIDQVSNLVESLSDBFYLDERREFEBIVKYANBLHIERNM 719  C3. NGTGKTDVKDYHIDQVSNLVESLSDBFYLDERREFEBIVKYANBLHIERNM 719	SULT 15  SULT 15  Alternate names: 135K insecticidal protein Alternate names: 135K insecticidal protein Alternate names: 135K insecticidal protein Alternate names: 135K insecticidal protein Becies: Bacilus thuringiensis Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09- Accession: Uncert.  Similar, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkaw File: Biol. Chem. 52, 1565-1573, 1988 File: Cloning and expression in Escherichia coli of the 135-kDa Accession: JT0241 Accession: JT0241 Accession: JT0241 Accession: JT16 cAHI> Cross-references: UNIPROT: P02965 Cross-references: UNIPROT: P02965 Cross-references: UNIPROT: P02965 Comment: The 135K protein has insecticidal activity against Plute Superfamily: parasporal crystal protein Keywords: delta-endotoxin	Query Match Best Local Similarity 43.3%; Score 1438.5; DB 2; Length 1176; Best Local Similarity 43.3%; Pred. No. 6.96-91; Matches 308; Conservative 117; Mismatches 226; Indels 61; Gaps 12;  Qy 36 NINHEDCLKMSEYENVE-FVSASTIQTGIGIAGKILGTLGVPFAGGVASLYS 87  4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLGLVD 62  Qy 88 FILGELWPKGKNQWEIEWEHVEBIINQKISTYARANKALTDLKGLGDALAVYHDSLESWG 147
Db 180 QRWGFDATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRTNGFRRELTLT 239  Qy 268 VLDLVALFPSYDTQWYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNAPSFS 323  Db 240 VLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFRGSAQ 285	Qy 324 AIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNMWGCHKLEFRIIGCTLNI 376	OY 437 FYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASHVKALVY 489  Db 396 LPSAVYRKSGTVDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGPSNSSVSIIRAPMF 453  OY 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGFFGDIRV 549	550 NINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIMNRGEDLDYK	Oy GTO RGLKTDVYDYHIOQVSNIVESLEDEFYLDEKRELFELYKYARELHIEKNW 719  RESULT 14  A22798  Parasporal crystal protein - Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis R;Shibano, Y; Yamagata, A; Nakamura, N; Iizuka, T.; Sugisaki, H; Takanami, M. R;Shibano, Y; Yamagata, A; Nakamura, N; Iizuka, T.; Sugisaki, H; Takanami, M. R;Shibano, Y; Yamagata, A; Nakamura, N; Iizuka, T.; Sugisaki, H; Takanami, M. R;Shibano, Y; Yamagata, A; Nakamura, N; Iizuka, T.; Sugisaki, H; Takanami, M. A; Reference number: A22798; MUID:85332070; PMID:2989108 A; Accession: A22798 A; MUID:85332070; PMID:2989108 A; Cosserences: UNIPROT:Q9SSV8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713 C; Comment: The authors translated the codon ACA for residue 264 as Ser. C; Superfamily: parasporal crystal protein C; Keywords: delta-endotoxin	Ouery Match  38.3%; Score 1439.5; DB 2; Length 934;  Best Local Similarity 43.3%; Pred. No. 4.1e-91;  Matches 308; Conservative 118; Mismatches 225; Indels 61; Gaps 12;  Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYS 87  4 NPNINEIPPRICESHPETENTETTOFFILISET-VPGAFVLGLUD 62  Qy 88 FILGELWPKGKNQWEIFWHVEEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWYG 147  Db 63 IIMGIFGPSQWDAFLVQIBQLINQKISFEREGLSNLYQIYABSFREWFA 119  QY 148 NRNNTRARSVVKSQYIALELMFVQKLPSFANGGEVPLLPIYAQAANLHLLLRABASIFG 207  DD 120 DPTNPALREBMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQANLHLLLLRABASIFG 207  QY 208 KEWGLSSSEISTFYNRQVERGEVPKYNSTGLNNLRGTNAESWVRYNOFRRDWTLM 267  180 QRWGFBAATINSRYNDTRLIGNYTDYAVRWYNTGLERRAWGPDSRDWVRYNOFRRDWTLM 289

268 VLDLVALFPSYDTOMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327 240 VLDIVALFSKYDTRYPIRTYSQLTREIYTNPV							
VLDLVALFESYDTQMYPIKTTAQLTREYY VLDIVALFESYDTQMYPIKTTAQLTREIY VLDIVALFSNYDSRRYPIRTVSQLTREIY AVVRNPHLLDFLEOVTIYSLLSRWSN RIEQNIRQPHLADILNSITIYTDVHRG TNTSINPVTLPFTSRDVYRTESL S AGNAAPPVLVSLTGLGIFRTLSSPLYRRI ASDNFYYPGYAGIGTOLQDSBNSLPPBAT FSTIXRQRGTVDSLDVIPPPQDN VYSWHTRSADRTNTIEPNSITOLPLYAAF TFSWQHRSABENNIIPSSQITQIPLYAAF TFSWQHRSABENNIIPSSQITQIPLYAAF TFSWQHRSABENNIIPSSQITQIPLYABF TFSWQHRSABENNIIPSSQITQIPLYABF TTPFSFLDVQSTFTIGAWNFSSGNEVYID TTPFFFSFLDVQSTFTIGAWNFSSGNEVYID TTPFFFSLDVQSTFTIGAWNFSGNEVYID NPRGLKTDVTDXHLDQVSNLVESLSDEFYIN NQIGLKTDVTDXHLDQVSNLVECLSDEFFC	327	381	397	450 547 510	570	667	
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Search completed: October 28, 2004, 18:31:52 Job time: 21.191 secs

Sequence

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Sequence 25, Appl Sequence 25, Appl Sequence 6, Appli Sequence 30, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli

US-09-178-252-25 US-09-826-660-25 PCT-US91-0560-4 US-09-661-322A-6 US-07-812-180A-2 US-08-315-480A-2 US-08-315-599-2 US-08-532-547-5 US-08-532-547-5 US-08-532-547-5 US-08-455-838-5 US-09-471-177-5 US-09-471-177-5

Sequence Sequence Sequence

-09-002-285-72 US-09-589-477-72

ALIGNMENTS

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STATE: 1100 New York Avenue, N.W.
CITY: Washington
CITY: Washington
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
APPLICATION NUMBER: US 07/52028
FILING DATE: OP-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: OP-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAMM: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION NUMBER: 70608/220720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08286870A

Patent No. 6663605

GENERAL INFORMATION:
APPLICANT: ELY, SH
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
ITLE OF INVENTION: BACTERIAL GENES
INUMBER OF SEQUENCES: 10
CORRESSEE: CUSHMAN DARRY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: Intellectual Property Group of
STREET: 1100 New York Avenue, N.W.
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TELEFAX: (202) 862-0944
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
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GY: linear
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TOPOLOGY:
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US-08-286-870A-8
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Sequence 4, An
Sequence 2, An
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(GGDZ 6/ptodata1/iaa/5A_COMB.pep:*
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(GGDZ 6/ptodata1/iaa/6A_COMB.pep:*
(GGDZ 6/ptodata1/iaa/6B_COMB.pep:*
(GGDZ 6/ptodata1/iaa/BCOMB.pep:*
(GGDZ 6/ptodata1/iaa/PCTUS COMB.pep:*
(GGDZ 6/ptodata1/iaa/backfiles1.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-661-322A-42
US-09-28-870A-4
US-09-218-942-2
US-08-286-870A-6
US-08-176-865-4
US-08-176-865-4
US-08-176-865-4
US-08-176-865-4
US-08-176-100-100
US-08-176-110-100
US-08-180-110-110
US-08-951-803-110
US-08-951-803-110
US-08-95-595A-7
US-08-468-7
US-08-468-7
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US-08-448-170-8
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                              Length 710;
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                                                                                                                                                DB 4;
                                                                                                                                              92.0%; Score 3459.5; DB 4; 92.1%; Pred. No. 2.2e-301; rative 16; Mismatches 32;
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                                    NAME/KEY: misc_feature
LOCATION: (200)
. LOCATION: (200)
. USER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
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GENERAL INFORMATION:
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APPLICANT: TALLOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GE
CORRESPONDENCES: 10
ADDRESSEE: CUSHMAN DARBY & CUG
Bacillus thuringiensis
                                                                                                                                                Query Match
Best Local Similarity 92.14
Matches 662; Conservative
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ORGANISM: 1
FEATURE:
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APPLICANT: Baum, James A.
APPLICANT: Chi.-Rei
APPLICANT: Chi.-Rei
APPLICANT: Chi.-Rei
APPLICANT: Chi.-Rei
APPLICANT: Bupar, Mark J.
APPLICANT: Rupar, Ma
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    Length 719;
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    DB 3;
    99.4%; Score 3739; D
Larity 99.4%; Pred. No. 0;
Conservative 2; Mismatches
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Patent No. 6593293
                           Similarity
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                             Best Local Sim
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      481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                      481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                          541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
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                                                                                                                                                                           601 TERTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYE 648
                                                                                                                                                                                                  601 TFRIVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPVEVTYE 648
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Mala, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
FILING DATE:
CLASSIETTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Score 3379; DB 2;
89.7%; Pred. No. 3.8e-294;
iive 34; Mismatches 40;
                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity 89.7
Matches 645; Conservative
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STREET: 30...
TTV: Raleigh
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STATE: NC
COUNTRY: US
ZIP: 27622
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US-09-003-217-2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
PILING DATE: 05-AUG-1994
PRING APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1999
ATPLICATION NUMBER: US-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.8%; Pred. No. 4.1e-295; Matches 647; Conservative. ~ 0; Mismatches 1;
3: Intellectual Property Group of
3: PILLSBURY, MADISON & SUTRO LLP
1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 76608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                        CITY: Washingtom.
STATE: DC
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 822-0944
INFORMATION FOR SEQ 1D NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
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MOLECULE TYPE: protein
                                 STREET: 1100
TTY: Washington
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           EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                              VDEHWKEVTHPIASDNEYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                          GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW
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                                                                                    TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08286870A; Sequence 6, Application US/08286870A; Parent No. 6063605
GENERAL INFORMATION:
APPLICANT: TAILOR, RH
APPLICANT: TIPETT, JM
APPLICANT: BACTERIAL GENES
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property Group of ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
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ZIP: 20005-3918
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
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09-MAY-1989
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APPLICATION NUMBER: US 07/
FILING DATE: 09-MAX-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 891.
FILING DATE: 09-MAY-1989
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US-08-286-870A-6
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Sequence 2, Application US/09218942

Patent No. 6232439

GENERAL INFORMATION:

APPLICATION Seacillus Thuringiensis Isolates with Broad Spectrum

TITLE OF INVENTION: Activity

TITLE OF INVENTION: Activity

TITLE OF INVENTION Activity

FILE REFERENCE: Cryli

CURRENT APPLICATION NUMBER: US/09/218,942

CURRENT FILING DATE: 1998-12-22

EARLIER PLING DATE: 1997-01-10

EARLIER FILING DATE: 1997-01-10

EARLIER FILING DATE: 1998-01-06

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTIN VEY: 2.0
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EEVPLLPIYAQAANLHLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWNN 240
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                                                                                                                               VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                                                            481 GSHVKALVYGWTHRSADRTWIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK
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                                                                 241 TGLNNLRAINGQSWVRYNQFRKDIELMVLDLVRVFPSYDILVYPIKITSQLTREVYIDAI
                                                                                                            GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
                                                                                                                                                                                   GCHKLEFRIIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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89.7%; Pred. No. 1.1e-293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.74
Matches 645; Conservative
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LENGTH: 719
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COUNTRY:
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Patent No. 5322687
GENERAL INFORMATION:
APPLICANT: Denovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: GONZALEZ JT., Jose M.
TITLE OF INVENTION: PACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
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                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                                Score 2795; DB 3; Length 535;
Pred. No. 6e-242;
0; Mismatches 1; Indels
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (202) 861-3000
TELEFPAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1601 Market Street, 36th Floor
Philadelphia
                                                                                                                                                                                                                74.3%;
                                                                                                                                                                                                           Query Match
Best Local Similarity 99.8 Matches 534; Conservative
                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                       ; MOLECULE TY:
US-08-286-870A-6
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US-08-100-709-4
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RTAGESTPFNFLNAQSTFTLGAQSFSN-QEVYIDRVEFVPAEVTFEAEYDLERAQKAVNA 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 LGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRATARLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 IGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 QAANLHILLIRDASLFGSEWGWASSDVNQYYQEQIRYTEEYSNHCVQWYNTGLNNLRGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 --INPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLIIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKALTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 HVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 SSNAKVDKISTDSLKN-ETDIELO-NINHEDCLKMSEYENVEPFVSASTIOTGIGAGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.8%; Score 2437.5; DB 1; Length
65.4%; Pred. No. 2.8e-209;
ive 90; Mismatches 141; Indels
                                                                                                                                                  Version #1.25
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
                                                                                                                                                                                                                                                                                                       Jhe.
27633
7205-49
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REPERRENCE/DOCKET NUMBER: 7205-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 65.4%
Matches 469; Conservative
                                                                                                                                                                                                                   19930729
                    ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-100-709-4
U.S.A.
                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
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RESULT 9
US-08-474-038-4

J US-08-474-038-4

J Sequence 4, Application US/08474038

J Sequence 4, Application US/08474038

J Setuct No. 5679343

GENERAL INFORMATION:
APPLICANT: Denovan, William P.
APPLICANT: Jan, Yuping
APPLICANT: Jan, Yuping
APPLICANT: Jose M.
TITLE OF INVENTION: PACILLUS THURINGIENSIS CTYET4 AND CTYET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
                                                                                                                                                                                                                                                                                                                                                      481 TLRAPVYSWTHRSADRINTIGPNRITQIPLVKALNLHSGVTVVGGPGFIGGDILRRINTG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                       RIVGETTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIBFVPVEVTYBABYDFBKAQEKVTA 662
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                                                                                                                                                                                                                  430 HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS 482
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                                  STIWYNNNAPSPSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNTQYMNMWGGHKLEFRII
                                                             GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT
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STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
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...GUIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC CD05/MS-D0S
SOFTWARE: PatentIn Release #1.0, Ve)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-UN-1995
CLASSIFTCATION: 514
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APPLICATION NUMBER: US 08/176,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLE, Christopher
REGISTRATION NUMBER: 27633
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TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Ganzalez Jr., Jose M.
TITLE OF INVENTION: DACILLUS THURINGIENSIS CLYET4 AND CLYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSES: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSES: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: O.S.A.
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663 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFELVKYANELHIERNM 719
                           13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGLAGKI
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Similarity 65.4%; Pred. No. 2.8e-209;
69; Conservative 90; Mismatches 141; Indels 17; Gaps
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APPLICATION NABER: US/08/176,865 FILING DATE: 30-DEC-1993 CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-75-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            Sequence 4, Application US/08176865
Patent No. 5616319
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TOPOLOGY: linear
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Sequence 4, Application US/08779046

Sequence 4, Application US/08779046

Sequence 4, Application US/08779046

Sequence 4, Application US/08779046

Patent No. 5854053

APPLICANT: Donovan, William P. APPLICANT: Tan, Yuping

APPLICANT: Jany, Christine S. APPLICANT: Jany, Christine S. APPLICANT: Jany, Christine S. APPLICANT: OF INVENTION: BACILLUS THURINGIENSIS cryff AND Cryff AND Cryff AND TILLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS INTHER OF SEQUENCES: S. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      71 LGTLGVPFAGQVASLYSFILGELWPKGKNOWEIFWEHVEEIINQKISTYARNKALTDLKG 130
                                                                                                                                                                                                                    67 LGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRNTAIARLEG 126
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                                                                                           Length 1229;
                                                                                                                       17;
                                                                                                                      141; Indels
                                                                                         64.8%; Score 2437.5; DB 1; 65.4%; Pred. No. 2.8e-209; ive 90; Mismatches 141;
           : 1229 amino acids
amino acid
3Y: linear
                                                                                                                   Matches 469; Conservative
SEQUENCE CHARACTERISTICS
                             ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-474-038-4
                                                                                                       Similarity
           LENGTH:
                                                                                                                                                                                                                                                       131
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT
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65.4%; Pred. No. 2.8e-209;
ive 90; Mismatches 141; Indels
A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENTING SYSTEM: RC-LUOS/NS-LUOS
SOFTWARE: PATENTIN RC-LUOS/NS-LUOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTONNEY/AGENT INFORMATION:
NAME: BG01c, Christopher:
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
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REFERENCE/DOCKET NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
Panitch Schwarze Jacobs & Nadel
                                                                                  STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 65.4
Matches 469; Conservative
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421.N.W. 41st Street, Suite A-1
                                                                                                             AESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
                                                                                                                                                                                                                                                                429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAANIHLILLIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250
                                                                                                                                     366
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127 LGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNBEVPLLMVYA 186
                                                                                                                                                                                                                                                                                                                                        HPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDBFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 TFGDIRLNINVPLSQRYRVRIRYASTIDLQFFTRINGTTVNIGNFSRIWNRGDNLEYRSF
                                                           483 HVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTG
                                                                                                                                                                                                                                                                GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT
                                                                                                                                                                                         STIWYNNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNIQYMNMGGHKLEFRTI
                                                                                                                                                                                                                                                                                                  367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF---
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0,
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APPLICATION NUMBER: US/08/448,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: David R. Saliwanchik
T: 2421 N.W. 41st Street, S
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08448170 Patent No. 5723758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Florida
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US-08-448-170-10
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STATE: F
COUNTRY:
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Sequence 4, Application US/08881340
Sequence 4, Application US/08881340
Sequence 4, Application US/08881340
Septemt No. 5942658
GENERAL INFORMATION:
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Golden S.
APPLICANT: Tan, Yuping
APPLICANT: Jose M.
TITLE OF INVENTION: DOIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                             RIVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA 662
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                                                                                                                                                           663 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIBRNM 719
                                                                                                                                                                               TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DESTREET PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-UN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2437.5; DB 2;
Pred. No. 2.8e-209;
); Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLÉ, Christopher
REGISTRATION NUMBER: 27633
REPERDICK/DOCKET NUMBER: 7205-49
TELEDHONE: 215-757-1590
INFORMATION FOR SEQ ID O: 4:
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65.4%; Pred
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Best Local Similarity 65.4%
Matches 469; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MOLECULE TYPE: protein US-08-881-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennsylvania
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVE: amino acid
TOPOLOGY: linest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                      RESULT 11
US-08-881-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: 1
STATE:
                                                                                   603
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181 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 QTGIGIVGKILGNLGVPFAGQVASLYSFILGELWPKGKSQWEIFWEHVEELINQKISTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
            Encoding Lepidopteran-Active Toxins
                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/961 001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.1%; Score 2335.5; DB 3;
89.5%; Pred. No. 8.9e-201;
iive 13; Mismatches 30;
                        STREET: Jay M. Sanders
STREET: 2411 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
ZJP.
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: US 07/759,247
FILING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: US 08/448,170
PRIOR APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: 39,355
FILING DATE: 37-MAY-1995
CLASSIFICATION NUMBER: 39,355
FILING DATE: 33-MAY-1995
CLASSIFICATION NUMBER: 39,355
FILING DATE: 330-MAY-1995
CLASSIFICATION NUMBER: 39,355
FILING DATE: 352,375-5800
FILING DATE: 322,375-5800
FILING DATE: 322,375-5800
FILING DATE: 322,375-5800
FILING DATE: 382,375-5800
                                                                                                                                                                                                                                                                31-OCT-1997
31-OCT-1997
31-OCT-1997
                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.5
Matches 445; Conservative
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TOPOLOGY: lir
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US-08-961-803-10
Sequence 10. Application US/08961803
Sequence 10. Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Steve
APPLICANT: Steve
ITILE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
ITILE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
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89.5%; Pred. No. 8.9e-201;
iive 13; Mismatches 30;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFTCATION: 4-24
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPERCENCE/DOCKET NUMBER: 31,794
REPERCENCE/DOCKET NUMBER: M/S 102D.C1
TELEPHONE: (904) 372-8800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERIFICS:
LENGTH: 488 amino acids
TYPE: amino acids
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Best Local Similarity 89.5
Matches 445; Conservative
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TOPOLOGY: lin
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APPLICANT: Koziel,
APPLICANT: Desai, N
APPLICANT: Lewis,
APPLICANT: Kramer,
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US-08-459-448A-7
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APPLICANT:
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TITLE OF INVENTION: SYNCHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
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STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/07951715A Patent No. 5625136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Duwson, John L.
                                                                                                                                                                                                                                             ASHVKALVYSWTHRSAD 497
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TELECOMMUNICATION INFORMATION:
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TELEPAX: (919)541-8689
INFORMATION FROR SEQ ID No. 7:
SEQUENCE: CHARACTERISTICS:
LENGTH: 1207 amino acids
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TOPOLOGY: linear
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US-07-951-715A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQ 572
                                                                                                                                                                                                                                                                                                                                                                                                    TOMYPIKITAQLIREVYIDAIGTVHPHPSFISTIWYNNNAPSFSAIEAAVVRNPHLLDFL 339
                                                        40 EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKN 99
                                                                                   10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 PFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSGNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 RTESLAGINLF--LTQPVNGVPRVDFHWKFVTHP----IASDNFYYPGYAGIGTQLQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573 PHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAMNFSSGNE
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                                                                                                                                                                                                                                  160 SQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIST
                                                                                                                                                                                                                                                                                                                   220 FYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYD
                    Gaps
                    13;
                    Indels
Pred. No. 1.7e-192;
; Mismatches 157;
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Levis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
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ilarity 64.0%; Pr
Conservative 77;
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OWEIFMEHVEEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 FYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 TOMYPIKTTAQLIREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFL 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVFFAGQLASFYSFLVGELWPRGRD
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SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.8%; Score 2250.5; DB 2; Length 64.0%; Pred. No. 1.7e-192; ive 77; Mismatches 157; Indels
                                                                      ADDRESSEE: No. 559336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-070-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 02-07/951,715
FILING DATE: US 07/951,715
APPLICATION DATA:
APPLICATION NUMBER: US 07/72,027
FILING DATE: 04-07-1991
ATTORNEY/AGENT INFORMATION:
NAME: PACE, GATY M.
RESTRENCE/DOCKET NUMBER: 40403
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CGITELECOMMUNICATION: TELEPHONE: (919)541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1207 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.0%
Matches 440; Conservative
  TITLE OF INVENTION: SYN
TITLE OF INVENTION: INV
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
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                                                                                                573 PHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNE 632
                                                                 633 VYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS
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Search completed: October 28, 2004, 18:34:16 Job time: 25.3343 secs

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WPI; 2001-123015/13
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Vincent JL,
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Aab66910 1
Aae36274 B
Aab66907 1
Adm74717 B
Aab66912 1
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Adk98484 E
Adk98489 E
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Adk98491 E
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                         2002273 seqs, 358729299 residues
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                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
                                                                                                   October 28, 2004, 17:51:02
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Gapop 10.0 , Gapext 0.5
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1 MKLKNQDKHQSFSSNAKVDK.
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Sequence:
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-	Aaw35259 Bacillus		먑	Aay30923 B. thurin	œ	Aaw44322 Bacillus	Aab19947 Bacillus	Aar50955 Bacillus	Aau02094 Bacillus	Aay31990 Chimeric	Aaw44321 Bacillus	Aab19950 Bacillus	Aau02046 B. thurin	Aay16796 Amino aci	Aau00421 B. thurin	Aau00420 B. thurin	Aab84628 Amino aci	Aau02039 B. thurin	Aay16797 Amino aci
AAR54074	AAW35259	AAW17699	AAW87633	AAY30923	ADK98479	AAW44322	AAB19947	AAR50955	AAU02094	AAY31990	AAW44321	AAB19950	AAU02046	AAY16796	AAU00421	AAU00420	AAB84628	AAU02039	AAY16797
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64.8	64.8	64.8	64.8	64.8	64.8	62.1	62.1	60.2	0.09	59.8	58.0	58.0	57.7	57.3	56.9	56.6	55.8	55.8	51.1
437	2437.5	2437.5	2437.5	2437,5	2437.5	2335.5		263	2258.5	2249.5	2180.5	2180.5	2171.5	2156.5	4	2127.5	2101	2101	1923.5
56	27	28	29	30	31	32	33	34	35	36	37	38	რ თ	40	41	42	43	44	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warner SAJ;
                                                                                                                                                                                                                              transgenic plant; insect-resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mackay EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cayley PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 57-59; 72pp; English.
AAB66909 standard; protein; 719 AA.
                                                                                                                                                                  Insecticidal protein cry1Ia3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-2000; 2000WO-GB002457.
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99GB-00030536.
                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 719; Conservative
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Lee MD;
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amino

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protein comprising an X-glycine motif as an active ingredient of a pesticide.

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal arrivity. The present sequence is sequence is used in the invention
                                                                                Claim 12; Page 47-50; 67pp; English
                      WPI; 2003-175137/17
                                            New insecticidal terminus, useful
                                                                                                                                                                                                                            Sequence 719 AA;
Vincent JL,
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             MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                               OTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
                                                              QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
                                                                                              RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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Length 719;
 100.0%; Score 3762; DB 6; 100.0%; Pred. No. 3.4e-294;
                            0; Mismatches
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Matches 719; Conservative
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B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crylla3

Insecticidal protein; pesticide; insecticidal crystal endotoxin;

Bacillus thuringiensis

12-DEC-2002

07-JUN-2001; 2001GB-00013900. 30-MAY-2002; 2002WO-GB002666

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant
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Lee MD;
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23-DEC-1999;
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Vincent JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Crylla; CrylBa; moth; butterfly; Colorado potato beetle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is B. thuringiensis (Bt) crystal protein Crylla, the DNA encoding which was muteted to allow cloning of domain III or domains I and II, to make the hybrid protoxins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYA 120
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99.7%; Pred. No. 1.8e-293;
ive 1; Mismatches 1;
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                                                                                              Bacillus thuringiensis partial mutant Crylla.
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/label= Signal_peptide
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/label= Mature_CrylIa
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             AAU02095 standard; protein; 719 AA
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                                                                    (first entry)
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nes 717; Conservative
                                                                                                                                                                   Bacillus thuringiensis.
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N-PSDB; AAS04855.
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                                                                                                                          Crystal
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8 g ∂ g à 30-MAY-2002; 2002WO-GB002666. 07-JUN-2001; 2001GB-00013900

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insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects f
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                                                                      Length 719;
                                                                                                    Indels
                                                                    99.7%; Score 3749; DB 4;
larity 99.7%; Pred. No. 3.8e-293;
Conservative 1; Mismatches 1;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiansis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Length 719;

Score 3749; DB 6; Pred. No. 3.8e-293;

99.7%;

Sequence 719 AA;

amino-

New insecticidal protein comprising an X-glycine motif e terminus, useful as an active ingredient of a pesticide

Claim 12; Page 53-56; 67pp; English

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protein, cryllas.

protein; pesticide; insecticidal crystal endotoxin; CRY.

Bacillus thuringiensis.

WO200298911-A2

B. thuringiensis insecticidal crystal endotoxin (CRY)

26-JUN-2003

AAE36275

AAE36275 standard; protein; 719

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                                                                                   GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW
                           TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crystal endotoxin (CRY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 44-47; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE36272 standard; protein; 719
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                                                                              TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
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                    RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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TRRIVGETIPESFLDVQSIFTIGAMNESSGNEVYIDRIBEVPVEVTYBAEYDFEKAQEKV
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Pred. No. 1.1e-292;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                        Insecticide; transgenic plant; insect-resistance
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Lee MD;
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Best Local Similarity
Matches 716; Conserv
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                                                                                                                                                                                                                                                                                                                                       Paecilomyces sp.
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1990-361486/48.

89GB-00010624

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The sequence carried on pJH12 which was isolated from B. thurin- giensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278) or bacteriophage EMB14 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-WAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                     Bacillus thuringiensis strains - used for producing an endotoxin for
protecting plants against insects, partic. Lepidoptera and Coleoptera.
 Bacillus thuringiensis; JHCC 4353
                                                                                                                                                                                                                                                               Claim 5; Fig 5-10; 66pp; English
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                                                                                                                                 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. sequence is used in the invention
                                                                                                          Gaps
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                                                                             Score 3743; DB 6;
Pred. No. 1.1e-292;
1; Mismatches 2;
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Best Local Similarity 99.6%;
Matches 716; Conservative
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                                                      Gaps
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                         Length 719;
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                         Score 3741; DB 2;
Pred. No. 1.7e-292;
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Best Local Similarity 99.4%;
Matches 715; Conservative 1
Sequence 719 AA;
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endotoxin deduced from DNA carried on pJH12

81 kD

(revised) (first entry) (revised)

24-OCT-2003 25-MAR-2003 27-FEB-1991

AAR08041;

Crystal; insecticide; toxin; delta endotoxin

ያ የ	541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMURGEDLDYK	ે દે	EEVPLLPIYAQAANLHLLLERDASIFQKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
3 8	1 to 0	a :	EEVPLLPIYAJAANLHLLLLKDASIFGKEMGLSSSBISTFYNRQVERAGDYSDHCVKWYS
Z QQ	601 TFXTVGFTTPFSLLDVQSTFTIGAMNFSSGNBVYIDRIEFVPVSVTYEABYDFEKAQEKV	o d	241 IGLNANARSWYRTNGFROWILDWOLDLYANFFSIDLOWITHIANGGEREVILDA 300
à	199	È	301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW 360
d d	661	qq	301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
RE	RESULT 9	δí	GCHKLEFRTIGGTLAISTOGSTNTSINPYTLPFTSRDVYRTESLAGINLFLTQPVNGVPR
<b>€</b> 81	Becolu AAB66910 standard; protein; 719 AA.	QQ D	GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
X S	AAB66910;	λo.	VDFHWKFVTHPIASDNFYYPGYAGIGTOLODSENELPPEATGQPNYESYSHRLSHIGEIS
X E	12-APR-2001 (first entry)	<u>ය</u> .	VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
S E S	Insecticidal protein crylla4.	8 1	ASHVKALVYSWTHRSADRTNTIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
{ }}	Insecticide; transgenic plant; insect-resistance.	qq	ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
X 8 3	Paecilomyces sp.	8 8	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWRRGEDLDYK
{ Z ;	WO200100841-A1.	an i	TGTFGDIRVNINPPFAQRYKVRIRYASTTDLQFHTSINGKALNQGNFSATWRRGEDLDYK
X E ;	04-JAN-2001.	ð i	TERTVGFTTPFSFLDVQSTFTIGAMNFSSGNBVYIDRIBFVPVBVTYBABYDFEKAQBKV
X F	23-JUN-2000; 2000WO-GB002457.	යු	TFRTVGFTTPFSFLDVQSTFT1GAWNFSSGNBVYIDRIBFVPVEVTYBAEYDFEKAQEKV
XKK	29-JUN-1999; 99GB-0001515. 23-DEC-1999; 99GB-00030536.	& g	661 TALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719 661 TALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDEFYLDEKRELFEIVKYANCHHIERNM 719
X & :	(ZENE ) ZENECA LTD.		
XX PPI	Griffin J, Carlile AJ, Cayley PJ, Mackay BA, Warner SAJ;	RESULT 10 AAE36274 ID AAE36	T 10 274 288 5274 standard: protein: 719 AA.
XX	WPI; 2001-123	XX	
XX	Novel insecticidal protein obtained	XX FI	26-JUN-2003 (first entry)
7 2 3	controlling insects production.	X E	B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crylla4.
4 23 X	Claim 14; Page 60-62; 72pp; English.	X &	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
{88		S S	Bacillus thuringiensis.
388	LION FACTIONYCES Sp. (See AABSSBY) to AABSBYUL and AABSBYUL). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for	X E X	WO200298911-A2.
8X		DX XX	12-DEC-2002.
SO	Sequence 719 AA;	PF	30-MAY-2002; 2002WO-GB002666.
	Query Match 99.4%; Score 3739; DB 4; Length 719; Best Local Similarity 99.4%; Pred, No. 2.4e-292.	{ E }	07-JUN-2001; 2001GB-00013900.
•	Conservative 1; Mismatch	\$ <b>2</b> 2	(SYGN ) SYNGENTA LTD.
ò	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIBLQNINHEDCLKMSBYENVEPFVSASTI 60	E X	Vincent JL, Viner R;
Q	н		WPI; 2003-175137/17.
કે ક	61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNOWEIFWEHVEEIINOKISTYA		New insecticidal protein comprising an X-glycine motif at the amino- terminus, useful as an active ingredient of a pesticide.
3 8	OL KIGIGLAGOKILDGILGGVERAGÇVASELISELEDGELMENGNENELENGELMENGALINGALSIIA.	S S	Claim 12; Page 50-53; 67pp; English.
e ć	121 KNYALI DINGLOGALAY TADSIESMYONKAN KAKSYYKSQI ALELAKYYYKLESFAYSG 180 121 RNYALTDLKGLGDALAYYHDSLESWYGNRNNTRARSVYKSQYI ALELMFYQKLPSFAYSG 180	\$888	The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are

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99.28;
                                                                             30-MAY-2002; 2002WO-GB002666
                                                                                                  07-JUN-2001; 2001GB-00013900
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Matches 715; Conservative
              Bacillus thuringiensis.
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                                                                                                                                                                  WPI; 2003-175137/17.
                                                                                                                       (SYGN ) SYNGENTA
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                                                                                                                                             Vincent JL,
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resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiens; insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
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Pred. No. 2.4e-292;
1; Mismatches 3;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify enter proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
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New insecticidal protein comprising an X-glycine motif a terminus, useful as an active ingredient of a pesticide.
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Pred. No. 1.2e-291;
1; Mismatches 2;
                                                                                                                          Claim 12; Page 42-44; 67pp; English
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Insecticidal protein; pesticide; insecticidal crystal endotoxin;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis cryl gene, expression vector, nucleotide sequence with high-toxicity to lepidoptera pests, encoded protein, primer sequences and the shuttle vector pSXX422b, useful as a pesticide.
      EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                       241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                           GTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHILDFLEQVTIYSLLSRWSNTQYMNWW
                                                                                                                                                                              361 GCHKLEPRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR
                                                                                                                                                                                                             VDFHWKEVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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                                                                                                                                                           361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxicity; lepidoptera; crylAb; crylBa; coleoptera; diptera;
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N-PSDB; ADM74716.
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                                                                     The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                   TALFTSTNPRGLKTDVKDYHIDQVSNIVESLSDEFYLDEKRELFEIVKYANBLHIERNM 719
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TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                   TPRIVGPITP PSFLDVQSTFTIGAWNFSSGNEVYIDRIEFV PVEVTYEAEYDFEKAQEKY
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Vincent JL,
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     The invention relates to a novel Bacillus thuringiensis cryl gene, gene combination, expression vector, nucleotide sequence of the B thuringiensis cryl gene with high-rexicity to lepidoptera pests and the amino acid sequence of the protein encoded by it, cooperative use of the cryl gene with the expression product of crylab or crylBa, primer sequences for expressing the genes, and the constructed shuttle vector pSX4422b. The gene in combination with the crylab or crylBa genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the cryllel protein.
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93.2%; Pred. No. 8.3e-276;
iive 27; Mismatches 22;
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92.5%; Pred. No. 2.6e-273;
tive 32; Mismatches 22;
                           transgenic plant; insect-resistance.
                                                                                                                                                                                          Mackay EA,
                                                                                                                                                                                           PJ,
                                                                                                                                                                                                                                                                                         Claim 14; Page 64-66; 72pp; English.
                                                                                                                                                                                            Cayley
                                                                                                                                      99GB-00015215.
                                                                                                                  23-JUN-2000; 2000WO-GB002457
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.55
Matches 665; Conservative
                                                                                                                                                                                           Carlile AJ,
Lee MD;
                                                                                                                                                                                                                            WPI; 2001-123015/13
                                                                                                                                                                                                                                                                                                                                                                                Sequence 719 AA;
                                                                                                                                                                      ZENE ) ZENECA
                                                                         WO200100841-A1
                              Insecticide;
                                                    Paecilomyces
                                                                                                                                       29-JUN-1999;
                                                                                                                                                                                            Griffin J,
Vincent JL,
                                                                                               04-JAN-2001
                                                                                                                                                                                                                                                                       production
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RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG

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540
                                                                                                                                                                      TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
                                                                                                                                                                                                                                                                                                                                                                   TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                           TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719

    B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crylibl.

                             TPRIVGFITPFSFLDVQSTFT1GAWNFSSGNBVY1DR1EFVPVBVTYEAEXDFEKAQEKV
                                                                                                                    TGTPGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New insecticidal protein comprising an X-glycine motif at terminus, useful as an active ingredient of a pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 56-58; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2001; 2001GB-00013900.
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Best Local Similarity 92.5
Matches 665, Conservative
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9 9 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA 120 

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1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI

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                                                                  121 RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVOKLPSFAVSG
                                                                                                            TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                            301 GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMW
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                                             EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSBISTFYNRQVERAGDYSYHCVKWYS
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                                                                                                                                                                            GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
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1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYANELHIERNM 719
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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SUMMAKLES		ΩI.	US-10-782-020-10	US-10-782-141-8	US-10-782-096-10	US-10-782-570-7	US-10-428-961-42	US-10-809-953-10	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23	US-10-428-961-38	US-10-614-524-2	US-09-826-660-25	US-10-089-678-1
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                RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                EEVPLLP1YAQAANLHLLLLRDAS1FGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                             TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI
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Bublication No. US20040197917A1

GBNERAL INPORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Carozzi, Nadine
APPLICANT: Carozzi, Nachael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: ARMI-0114, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274143
CURRENT APPLICATION UMBER: US/10/782,141
CURRENT APPLICATION NUMBER: 60/448,632
PRIOR APPLICATION NUMBER: 60/448,632
PRIOR PILING DATE: 2003-02-20

PRIOR FILING DATE: 2003-02-20
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Best Local Similarity 99.6%; Pred. No. 3.7e-307;
Matches 716; Conservative 1; Mismatches 2;
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 719
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CRGANISM: Bacillus thuringiensis
US-10-782-141-8
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QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGRNQWEIFWEHVEELINQKISTYA
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APPLICANT: Carcat, Nadine
APPLICANT: Carcat, Michael
APPLICANT: Carcat, Michael
APPLICANT: Koziel, Michael
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274148
FILE REPERENCE: 045600/274148
CURRENT APPLICATION NUMBER: 40/448,633
PRIOR PILLING DATE: 2004-02-19
PRIOR PILLING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ ID NO. 10
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US-10-782-096-10
'Sequence 10, Application US/10782096
'Publication No. US20040210964A1
'GENERAL INFORMATION:
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US-10-782-096-10
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7
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US-10-428-961-42
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                                                            MALKNODKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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Sequence 7, Application US/10782570

Fublication No. US20040210965A1

GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Cariel, Michael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AKMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AKMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AKMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AKMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AKMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AVENDER: US/10/782,570
CURRENT APPLICATION NUMBER: US/10/782,570
CURRENT FILING DATE: 2003-02-09

PRIOR FILING DATE: 2003-02-09

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0
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    Pred. No. 3.7e-307
1; Mismatches 2
 99.68;
                716; Conservative
Best Local Similarity
Matches 716; Conserv
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APPLICANT: Baum, James A.

APPLICANT: Baum, James A.

APPLICANT: Chu, Chin-Rei

APPLICANT: Chu, Milliam P.

APPLICANT: Glimer, Amy J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Legidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polymucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1
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                                                                                                                                                      1 MKLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSBYENVEPFVSASTI
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  719;
  Length
                                                          Indels
Score 3743; DB 17;
Pred. No. 3.7e-307;
1; Mismatches 2;
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CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
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Publication No. US20030237111A1
GENERAL INFORMATION:
  99.5%;
  Query Match
Best Local Similarity 99.6'
Matches 716; Conservative
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APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Henk
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC
TITLE OF INVENTION: RESCOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC
TITLE OF INVENTION: RESCOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC
TITLE OF INVENTION: RESPONSE: 021565-078
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US/09/661,016
PRIOR APPLICATION NUMBER: US/09/661,016
PRIOR FILING DATE: 1990-05-30
PRIOR FILING DATE: 1990-05-31
PRIOR FILING DATE: 1989-05-31
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NO 1: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 THP-----IASDNFYYPGYAGIGTQLQDSENELPPEATGOPNYESYSHRLSHIGLISASH
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60.2%; Score 2263.5; DB 16; Lengt
Best Local Similarity 62.4%; Pred. No. 1e-181;
Matches 447; Conservative 79; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10
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              Botterman, Johan
Van Rie, Jeroen
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                                                                                                                                                                NAME/KEY: misc feature; LOCATION: (200)...(200); OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amin US-10-428-961-42
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                                                                                                                                                                                                                                                        Query Match 92.0%; Score 3459.5; DB 14; Length 710; Best Local Similarity 92.1%; Pred. No. 3.4e-283; Matches 662; Conservative 16; Mismatches 32; Indels 9;
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 42
LENGTH: 710
                                                                                                                          TYPE: PRT
ORGANISM: Bacillus thuringiensis
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RESULT 6
US-10-809-953-10
is Sequence 10, Application US/10809953
ipublication No. US20040181825A1
igeneral information:

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JOHNEAN INTEGRATION OF THE PARTICANT CHU, Chin-Rei

APPLICANT Chu, Chin-Rei

APPLICANT Chu, Chin-Rei

APPLICANT Chu, Chin-Rei

APPLICANT Choovan, William P.

APPLICANT Choovan, William P.

APPLICANT Choovan, Mark J.

TITLE OF INVENTION Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION PROPER. US/10/428,961

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

FENCET.
                                                                                                                                                                                                                                                                                                                                    308 EQLIIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGAINTSINPVTLRFASRDVY 367
                             160 SQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIST 219
                                                                                                                                                                                                             280 TOMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFL 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512
                                                          424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQIPM
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Publication No. US20030237111A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 421; Conserv
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FININPRRIKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
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                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.30
RRENT APPLICATION DATA:
PLING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION PATA:
IOR APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 2250.5; DB 10; Length; Pred. No. 1.3e-180; 77; Mismatches 157; Indels
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FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UN-1992
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPONDENCE ADDRESS:
DADRESSES: Syngenta Biotechnology,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERROCE/DOCKET NUMBER: S-188051
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; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7
                                                                                                                                                                                                                                                                                                                      Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
F INVENTION: SYNTHETIC DI
                                                                                                                                                                             APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
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                                                                                                             Sequence 7, Application US/09988462
Publication No. US20030046726A1
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al Similarity 64.0%;
440; Conservative 7
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF
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                                                                    RESULT 7
US-09-988-462-7
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242 IRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRTNA 301
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                                                               KFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGOPNYESYSHRLSHIGLISASHVK 485
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                       61
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Patent No. US20010026940A1

GENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Navary Kenneth E.

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1

CURRENT PELING DATE: 2001-04-05

PRIOR FILING DATE: 1994-10-23

PRIOR PAPLICATION NUMBER: 60/076,445

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1998-03-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 23

LENGTH: 1186
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                                                 IACKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYARNKAL
                                                                                                                                                        LPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNN
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                                                                                                    TDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPL
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US-09-826-660-23
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TYPE: PRT ORGANISM: Artificial Sequence

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Sequence 38, Application US/10428961
Publication No. US20030237111A1
General INFORMATION:
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                                                                                                                                                                                                                                                                LPIYAQAANLHLLLLRDASIFGKEWGLSSSBISTFYNRQVERAGDYSYHCVKWYSTGLNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 PSGFASTNWFNNNAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNWHRL
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                                                                                                       Length 1186;
                                                                                                                                                               Indels
                                                                                                 tch al Similarity 58.7%; Pred. No. 1.1e-172; 419; Conservative 107; Mismatches 175;
; OTHER INFORMATION: Toxin encoded by synthetic B.t. US-09-826-660-23
                                                                                                           Query Match
Best Local Similarity
Matches 419; Conserv
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                                                                                                     Bacillus thuringiensis
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                                                                                                 from
APPLICANT: Vanneste, Stijn
APPLICANT: Van Rie, Jeroen
TITLE OF INVENTION: Insecticidal proteins fro
FILE REFERENCE: NEWEYSUS.
CURRENT APPLICATION NUMBER: US/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2
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Best Local Similarity 59.2
Matches 422, Conservative
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        PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 38
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Publication No. US20040016020A1
GENERAL INFORMATION:
APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
APPLICANT: Mathieu, Eva
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Bacillus thuringiensis
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APPLICATE: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: DF 2000-236140
PRIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR PRING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           45.4%; Score 1707.5; DB 14; Lengt
47.6%; Pred. No. 9.8e-135;
iive 125; Mismatches 221; Indels
                                                                  Sequence 1, Application US/10089678 Publication No. US20030017967A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 47.6%; Pr
Matches 359; Conservative 125;
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       Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardinacau, Guy A.
APPLICANT: Cardinacau, Guy A.
APPLICANT: Cardinacau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR PRIOR TILING DATE: 1998-0-3-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
SSETURNOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 SSNAKVDKISTDSLKN-----ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSGFASTIWFINNAPSFSAIEAAVIRPPHLLDFPEQLIIFSVLSRWSNIQYMNYWVGHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASHVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%; Score 1923.5; DB 9; Length 643; llarity 57.5%; Pred. No. 2.1e-153; Conservative 100; Mismatches 160; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 GFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYE 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25
Sequence 25, Application US/09826660
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 370; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 EYSDYCVKWYKIGLDKLKGTTSKSWLNYRQPRREMTLLVLDLVALFPNYDTHMYPIETTA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLTREVYTDAIGTVHPHPSFTST----TWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 QLTRDVYIDPIA----FNIVISIGFCNPWSTHSGILFYEVENNVIRPPHLEDILSSVEIN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 SLLSR----WSNTOYMONMGGHKLEFR----TIGGTLNISTOGSTNTSINPVTLPFTSR 396
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   530 INRNNGNIQNRGYIEVPIQFTSTRYRVRVRYRASVTSIELNVNLGNSSIFTNTLPATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 VEPFVSASTIQTGIGLAGKILGTLGVPFAGQVASLYSFILGELWP-KGKNQWEIFWEHVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAG
                                                                                                     593 RGEDLDYKTFRTVGFTTPFSFLDVQSTFT----IGAWNFSSGNEVYIDRIEFVPVEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQNINHEDCLKMSEYE----N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.0%; Score 1655.5; DB 17; Length 1157; 48.8%; Pred. No. 2.4e-130; ive 97; Mismatches 233; Indels 57;
                                                                                                                                                                                                                                                                                                         APPLICANT: datogat, nucleon APPLICANT: Hargiss, Tracy APPLICANT: Hargiss, Tracy APPLICANT: Hargiss, Tracy APPLICANT: Carr, Nichael G. APPLICANT: Carr, Brian APPLICANT: Carr, Brian TITLE OF INVENTION: AAWA-014, A Delta-Endotoxin Gene and TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION WURBER: US/10/782,141 CURRENT FILING DATE: 2004-02-20 FRIOR FILING DATE: 2004-02-20 FRIOR FILING DATE: 2003-02-20 NUMBER OF SEQ ID NOS: 23 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16
                                                                                                                                                                                                                              RESULT 15
US-10-782-141-16
US-10-782-141-16
Sequence 16, Application US/10782141
Publication No. US20040197917A1
GENERAL INFORMATION
APPLICANT: Garczzi, Nadine
APPLICANT: Hargiss, Tracy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                           647 YEAEYDFEKAQE 658
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641 FEVEYDLERAQK 652
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Best Local Similarity 48.8
Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAESWVRYNQFRRDMILMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAIGTVHPHPSF 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
44.6%; Score 1678.5; DB 14; Length
Best Local Similarity 51.5%; Pred. No. 1.1e-132;
Matches 346; Conservative 105; Mismatches 174; Indels
                                                                          NLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                          , TYPE: PRT
, ORGANISM: Bacillus thuringiensis
US-10-428-961-6
 626
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523 SYKITQIPAVKGDMLYLGSYVVQGPGFFFGGDILKRINDSI 564 RYASTTDLQFHTSINGKAINGGNFSATWRGEDLDYKTFR 64 RYASTTDFEF-TLYLGDTIEKNRFNKTMDNGASLTYETFR 583 RYASTTDFEF-TLYLGDTIEKNRFNKTMDNGASLTYETFR 624 AWNFSGGNEVYTDRIEFVPVEVTYEAEYDFEKAOEKVTAL	504 PNSITQIPLVKAFNLGSGAAVVRGPGFTGGDILRRTNTGT:	466 SSDEIPLDRI-VEVAESYSHRLSHITSHSFSKNGSAYY 504 PNITQIPLVKAFNLSSGAVVRGPGFTGGDILRRINTGTI 523 SDKITQIPAVKGDMLYLGGSVVQGPGFTGGDILKRINPSII 564 RYASTTDLOFHSINGKAINQGNFSAFWRGEDLDYKTFRF 664 RYASTTDFFF-TLYLGDTIERGNFNKTWDNGASLTYFFR 683 RYASTTDFFF-TLYLGDTIERGNFNKTWDNGASLTYFFFK 664 AWNFSGGNEVYIDRIBFVPVEVTYBAEYDFEKAOEKVTALI	452 SENELPPEATGQPNYESYSHRLSHIGLISASHVI  466 SEDEIPLDRT-VPVAESYSHRLSHITSHSFSKNG-SAYYGS 504 PNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFF 523 SPKITQIPAVKGDMLYLGGSVVGOFTGGDILKRTNPSILC 54 RYASTTDLOPHTSINGKAINGUPSATWNRGEDLDYKTFRT 583 RYASTTDFEF-TLYLGDTIEKNRFNKTMDNGASLTXETFKF, 583 RYASTTDFEF-TLYLGDTIEKNRFNKTMDNGASLTXETFKF,	DIFEINSTVANLANYYÇKAYĞHYPGSWHHMÜKR SENELPPEATGOPNYESYSHRLSHITG SSDEIPLDRT-VPVAESYSHRLSHITSHSFSKNG PNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR SPKITQIPAVKGDMLYLGGSVYQGPGFTGGDILR SDKITQIPAVKGDMLYLGGSVYQGPGFTGGDILK KAKSTTDLQFHTSINGKAINGGNFSATWARGEDL RYASTTDLQFHTSINGKAINGGNFSATWARGEDL RYASTTDFEF-TLYLGDTIEKARFNKTMDNGASL	::  revno 700
					624 AWNESSGNEVYIDRIEFVPVEVTYEAEXDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQ 
					DYKTERTVGFTTPFSFLDVQS:  :  :
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Search completed: October 28, 2004, 18:41:02 Job time : 71.6795 secs

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Tounsi S., Zouari N., Jaoua S.;
Tounsi S., Zouari N., Jaoua S.;
Tounsi S., Zouari N., Jaoua S.;
Tounsi S., Zouari N., Jaoua S.;
Enclius and study of the expression of a novel crylla-type gene Bacillus thuringiensis subsp. kurstaki.";
J. Appl. Microbiol. 95:23-28(2003).
EMBL; AJ315121; CAC85964.1;
SEQUENCE 719 AA; 81203 MW; 8676E5AGC25DAFE8 CRC64;
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                                                                                                                                                                                                                                                                                                                  Tailor R., Tippett J., Gibb G., Pelle S., Pike D., Jordan L., Ely S., "Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."; Mol. Microbiol. 6:1211-1217(1992).
                VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                   421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                        TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformaties and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-> Y (in strain JHCC4835 and strain HD-
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Selvapandiyan A., Bhatnagar R.K.;

"Isolation, cloning and expression of cryV gene.";

"Isolation, cloning and expression of cryV gene.";

submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-pithelial cells of certain coleopteran and lepidopteran species.

epithelial cells of certain coleopteran and lepidopteran species.

-!- FUNCTIONENTAL STRABS: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
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KQ -> NE (in strain HD-1 and strain 61)

3627E5A6C25DAFF5 CRC64;
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    -!- SIMILARITY: Belongs to the delta endotoxin family.

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Pred. No. 7.2e-252;
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EMBL; X62821; CAA4633.1; --
EMBL; 136391; AAB00999.1; --
EMBL; Y08920; CAA70124.1; --
EMBL; Y08920; CAA70124.1; --
EMBL; Y08920; CAA70124.1; --
EMBL; X55383; S25583.
HSSP; PO2965; ICIY.
INCEPPO; IPRO01978; ENGOLOXIN.
INCEPPO; IPRO05639; endotoXIN.
INCEPPO; IPRO08979; Gal bind like.
FEan; PF03944; EndotoXIN.
PEan; PF03945; EndotoXIN.; 1.
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719 AA; 81216 MW;
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                                                                                                  GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
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     TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                 241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-T01 328;
Bepindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
Complete sequence of cryll gene of isolate T01 328 from thuringiensis from Cubateo (SP - Brazil) soil.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX262167; AAP86782.1;
SEQUENCE 719 AA, 81216 MW; 3627E5A6C25DAFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
Bacillus cereus group.
NCBI_TaxID=1428;
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AAP86782;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 7.2e-252;
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Local Similarity 99.6%;
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99.5%; Score 3743; DB 2; Length 719;
Best Local Similarity 99.6%; Pred. No. 7.2e-252;
Matches 716; Conservative 1; Mismatches 2; Indels (
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SEQUENCE FROM N.A.

SEBUIDOLA R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
Submitteed (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY262167; AAP86702.1; -.

InterPro; IPRO01178; Endotoxin.

InterPro; IPRO08503; endotoxin.

InterPro; IPRO08503; endotoxin.

InterPro; IPRO08503; Endotoxin.C; 1.

R Pfan; PP03944; Endotoxin.C; 1.

R Pfan; PP03945; Endotoxin.M; 1.

R Pfan; PP03945; Endotoxin.M; 1.

R Pfan; PP03945; Endotoxin.N; 1.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI TaxID=1428,
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                                                                   RNKALTDLKGLGDALAVYHDSLBSWVGNRNNTRARSVVKSQYIALELMPVQKLPSFAVSG
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                                                                                                                            BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
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SLORG Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076953; AAC26910.1; -
HSSP; P02965; ICIY.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:000552; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR008639; endotoxin.
InterPro; IPR008639; endotoxin.
InterPro; IPR008639; endotoxin.
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plasmid large plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29339;
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SONG F., Zhang J., Gu A., Huang D., Li G.;
Song F., Zhang J., Gu A., Huang D., Li G.;
Song F., Zhang J., Gu A., Huang D., Li G.;
Submitted (APR-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AR373207; AAK66742.1; -
R GO, GO.0005102; Preceptor binding; IEA.
GO, GO.0005102; Preceptor binding; IEA.
GO, GO.0006502; Preceptor binding; IEA.
GO, GO.0006502; Preceptor binding; IEA.
InterPro; IPRO0178; Endotoxin.C.
InterPro; IPRO05639; endotoxin.N.
InterPro; IPRO05639; endotoxin.N.
InterPro; IPRO05639; Endotoxin.N.
R Pram; PR03944; Endotoxin.M; 1.
R Pram; PR03945; Endotoxin.M; 1.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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nes 715; Conservative
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

REMBL; AF278797; AAM73516.1; ...

RESP; P02965; LITY.

GO; GO:0005102; F:receptor binding; IEA.

GO; GO:000552; P:petfense response; IEA.

RICEPTO; IPRO06539; endotoxin.

RILEPTO; IPRO0539; endotoxin.

RILEPTO; IPRO0539; endotoxin.

RILEPTO; IPRO0553; endotoxin.

RILEPTO; IPRO0553; endotoxin.

RILEPTO; IPRO0553; endotoxin.

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REAM; PF03944; Endotoxin.

REAM; PF03945; Endotoxin.

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REAM; PF03945; Endotoxin.N; 1.
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                                                                                                             719 AA; 81230 MW; 42746D478359BBA7 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                        99.3%; Score 3737; DB 2;
99.4%; Pred. No. 1.9e-251;
1ive 1; Mismatches 3;
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O1-OCT-2002 (TrEMBLrel. 22, Last seq
O1-MAR-2004 (TrEMBLrel. 26, Last and
Cry.
Bacillus thuringiensis,
Bacteria, Firmicutes; Bacillales; Ba
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Porcar M., Martinez C., Caballero
        Endotoxin_C; 1.
Endotoxin_M; 1.
Endotoxin_N; 1.
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Best Local Similarity 99.4
Matches 715; Conservative
     Pfam, PF03944; E
Pfam, PF00555; E
Pfam, PF03945; E
Plasmid.
                                                                                                             SEQUENCE
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         TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%; Score 3503; DB 1; 92.5%; Pred. No. 3.7e-235; iive 32; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 107642; AAAB114.1; -...
PIR; 140590; 140590.
HSSP: P02056; 1CIY.
INCEPPO: IPRO0178; ENDOLOXIN.
INCEPPO: IPRO05639; endotoXIN.
INCEPPO: IPRO05639; endotoXIN.
INCEPPO: IPRO08639; endotoXIN.
INCEPPO: IPRO08639; endotoXIN.
Pfam; PF03944; EndotoXIN.C; 1.
Pfam; PF03945; EndotoXIN.1.
Pfam; PF03945; EndotoXIN.N; 1.
Pfam; PF03945; EndotoXIN.N; 1.
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SEQUENCE 719 AA;
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SEQUENCE FROM N.A.
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Best Local S:
Matches 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGHRLEFRTIGGVLNTSTQGSTNTSINPVTLPFTSRDVXRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIBLQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                     "Identification of cryll-type genes from Bacillus thuringiensis strains and characterization of a novel cryll-type gene.";

Appl. Environ. Microbiol. 69:5207-5211(2003).

R BMBL; AFC11190; AAG435C6.;

C GO:0001102; Preceptor binding; IEA.

R GO; GO:00016102; Preceptor binding; IEA.

R GO; GO:0005405; Preceptor binding; IEA.

R GO; GO:0005405; Preceptor binding; IEA.

R InterPro; IPR0019178; Endotoxin.

R InterPro; IPR00538; endotoxin.

R InterPro; IPR005538; endotoxin.

R InterPro; IPR00553; endotoxin.

R InterPro; IPR00555; Endotoxin.C; I.

R Pfam; PF00394; Endotoxin.C; I.

R Pfam; PF00555; Endotoxin.M; I.
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                                                                                                                                                  Gu A., Wu Y., Han L., He K., Chen Z., Yao
                                                                                                                                                                                                                                                                                                                                                                                      Length 719;
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                                                         Bacillus thuringiensis.
Plasmid pBTC19.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                 719 AA; 81024 MW; 7E17481922C435E6 CRC64;
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                     93.9%; Score 3534; DB 2; 93.2%; Pred. No. 2.6e-237; cive 27; Mismatches 22.
                                                                                                                              STRAIN=BTC007;
MEDLINE=22837682; PubMed=12957903;
                                                                                                                                                                                                                                                                                                                                           Pfam; PF03945; Endotoxin_N; 1.
   (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                             670; Conservative
                                                                                                                                                     Song F., Zhang J., Gu A.
Hu Y., Li G., Huang D.;
"Identification of cryll
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                   SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=1428;
                           01-MAR-2004
    01-MAR-2001
01-MAR-2001
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-i- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-i- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of certain coleopteran and lepidopteran species.

Active on Plutella xylostella but non Bombyx mori.

-i- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                                            TERTVGFTTPFSFSDVQSTFTIGAMNFSSGNBVYIDRIBFVPVBVTYBABYDFEKAQBKV
    TERTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
65-JUL-2004 (Rel. 44, Last annoin update)
Pesticidial crystal protein cryllb (insecticidal delta-endotoxin Cryll(b)) (Crystaline entomocidal protoxin) (81 kDa crystal protein) Name-cryllb, Synonyms-cryll(b), cryv, cryv465; Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                       TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                                                                                                                                                                                                                          661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM
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-!- MISCELLANEOUS; Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95314293; PubMed=7793960; Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryv-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
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    -!- SIMILARITY: Belongs to the delta endotoxin family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFRTVGFTTPFSFLDVQSTFT1GAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTGIGIAGKILGNPGVPFAGQVASLYSFILGELWPKGKSQWEIFMEHVEELINQKISTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNKALADLKGLGDALAVYHESLESWIENRNNTRVRSVVKNOY1ALELMFVQKLDSFAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSESEISTFYNRQSSQTQEYSDYCSEWYN
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                        of the protein is located
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                                         terminus.
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89.4%; Pred. No. 1.4e-226;
iive 36; Mismatches 40;
                                                                                                                                                                                                                                                                                                                             endotoxin_C.
endotoxin_N.
Gal_bind_like.
                                                                                                                                                                                                                                                                                    HSSP; P02965; 1CIY.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_lik
Pfam; PF03944; Endotoxin.C; IPR0055; Endotoxin.M; I.
Pfam; PF03945; Endotoxin.M; I.
                   MISCELLANEOUS: Toxic segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              719 AA; 81403 MW;
                                                                                                                                                                                                                                                                  EMBL; AF047579; AAD44366.1; -. HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 89.4
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DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 44, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)

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Gurr. Macrobiol. 41:65-69(2000).

-!-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!-FUNCTION: Promotes of many lepidopteran larvae. Active on Plutella
epithelial cells of many lepidopteran larvae. Active on Plutella
xylostella and on Bombyx mori.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                                                 QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFWEHVEEIINQKILTYA
                                                                                                                                            EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASBISTFYNRQVERTRDYSDHCIKWYN
                                                                                                                                                                                                                                                                                                         GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWW
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                                                                                                                    RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

RA Tacillus thuringiensis cryet4 and cryet5 toxin genes and proteins

RT toxic to lepidopteran insects.";

RL Patent number US5322687, 21-JUN-1994.

C. -! FUNCTION: Promotes colloidosmocic lysis by binding to the midgut

C. -: FUNCTION: Promotes colloidosmocic lysis by binding to the midgut

C. -: DEVELOPMENTAL STAGE: The crystal protein is produced during

CC -: DEVELOPMENTAL STAGE: The crystal protein is produced during

CC -: DEVELOPMENTAL STAGE: The crystal protein is located in the N-

LA STALLA STAGE: COST. L. COMMENT OF the protein is located in the N-
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                                                                                                                                                                                                                                                                                                                         GSHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGHILRRTK 540
                                                                                                                                                                           361 GGHRLESRÞIGGALNTSTÓGSTNTSINÞVTLOFTSRDFYRTESWAGINLFLTOPVNGVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 TERTVGETTPESFSDVQSTFTIGAWNFSSGNEVYIGRIBEVPVEVTYBAEYDFEKAQBKV
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30-MAY-2000 (Rel. 39, Last sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllb (Insecticidal delta-endotoxin CryIB(b)) (Gryetaline entomocidal protoxin) (140 kDa crystal protein)
                                                                                          VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                                                                                                                                             TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                   421 VDFHWKFPTLFIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                                                                      481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
TGINNLRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                     GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
                                                                                                                                           GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmičutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=crylBb; Synonyms=crylB(b), cryBT5;
Bacillus thuringiensis.
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HSSP; P02965; 1CIY.
InterPro; IPR001178; Endotoxin.
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                         RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVYKSQYIALELMFVQKLPSFAVSG
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C18 / EGYPt;
Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
Submitted (MAR.1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
     TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDBKRELFEIVKYANELHIBRNM
                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllc (Insecticidal delta-endotoxin Cryll(c)) (Crystaline entomocidal protoxin) (81 kDa crystal protein)
Name=cryllc; Synonyms=cryll(c);
Bacillus thuringiensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            epithelial cells of insects.
DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: Toxic segment of the protein is located in the
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                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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81210 MW; 8370B3F06B905DFF CRC64;
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Pred. No. 1.6e-226;
1; Mismatches 40;
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HSSP, P02965, 1CIY.
InterPro, IPR001178, Endotoxin.
InterPro, IPR005638, endotoxin_C.
InterPro, IPR005638, endotoxin_C.
InterPro, IPR008979, Gal_bind_like.
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Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
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087404;
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483 HVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTG 542
  Firmicutes; Bacillales; Bacillaceae; Bacillus
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469; Conservative
                                                                                                                                                                                                                                                                                                                             1233 AA;
                           FROM N.A.
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SEQUENCE 12
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C1BC. BACTM STANDARD; PRT; 1233 AA.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
Pesticidial crystaline entomocidal protoxin) (140 kDa crystal protein).
Name=crylBc; Synonyms=crylB(c), crylBc;
Bacillus thuringiensis (subsp. morrisoni).
                                                                                                                                    TLRAPVYSWIHRSADRINIIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRINIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIVGFTTPFSFLDVQSTFT1GAWNFSSGNEVY1DR1EFVPVEVTYEAEYDFEKAQEKVTA
                                                                                                                        SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIAGKI
                                                                                                       Gaps
                                                                                                      17;
                                                                                    Length 1229;
                                                                                                       Indels
                                                                1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
                                                                                    DB 1;
                                                                                                      90; Mismatches 141;
                                                                                    Score 2437.5; DB 1,
Pred. No. 1.3e-160;
         endotoxin_N.
Gal_bind_like.
                          Pfam; PF03944; Endocoxin_C; 1.
Pfam; PF00355; Endocoxin_M; 1.
Pfam; PF03945; Endocoxin_N; 1.
Sporulation; Toxin. N; 1.
                                                                                    64.8%;
                                                                                             65.4%;
                                                                                             al Similarity 65.4
469; Conservative
         IPR005639;
IPR008979;
          InterPro;
InterPro;
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CIBC BACTM
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DT 30-MAY.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
                                                                                                                                                                                                                        the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1233;
                                                                                                                                                                                          98
                                                                                                                     epithelial cells of insects.
DEVELOPMENTAL STAGE: The crystal protein is produced dur sporulation and is accumulated both as an inclusion and
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                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the delta endotoxin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.8%; Score 2437.5; DB 165.4%; Pred. No. 1.4e-160; ive 90; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin.M.
IPfam; PF03945; Endotoxin.M. 1.
Pfam; PF03945; Endotoxin.N. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140451 MW;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  SMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88203216; PubMed=3362680;
Brizzard B.L., Whiteley H.R.;
Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis.";
Nucleic Acids Res. 16:2723-2723(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              part of
                                                                                                                                                                                             FGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFR
                                                                                                                                                                                                            VKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGT
                                                                                                                                                    604 TVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTAL
                                                                                                                                                                                                                                                                                                      GCTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLF--LTQPVNGVPRVDFHWKFV
                                            THP----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta-endotoxin
kDa crystal protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the midgut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
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CIBA BACTK
AC POSSI7; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1904 (Rel. 34, Last annotation update)
DT 05-UUL-2004 (Rel. 34, Last annotation update)
DT 05-UUL-2004 (Rel. 35, Last sequence update)
DT 07-YID (A) (Crystall ne protein crylas (Insecticidal delta-endot DE CrylE(a)) (Crystall ne protein crylas (Insecticidal protoxin) (140 kDa crystal DE Sacillus thuringiensis (Subsp. kurstaki), and OS Bacillus thuringiensis (Subsp. entomocidus).

OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN III TaxID=29339, 1436;
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SPECIES=B.t.entomocidus; STRAIN=HD-110;
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SEQUENCE FROM N.A.
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                                                                                                                                                                          660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNL 716
    RIVGFITPPSFLDVQSIFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA
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                                               TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-cry1Ba2;
Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=HD-9;
Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
Submitted (MAR-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AF183025; AAK51084.1; --
                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-WAR-2004 (TrEMBLrel. 26,
Delta-endotoxin CrylBa2.
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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STIWYNNAPSESAIEAAVVRNPHLIDFIEQVIIYSLLSRWSNTQYNNWWGGHKLEFRII 370
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        HSSP, P07130, DDC.

A InterPro; IPR001178; Endotoxin.

A InterPro; IPR005639; endotoxin.

R InterPro; IPR005639; endotoxin.

R InterPro; IPR008979; Gal bind like.

Pfam; PF003944; Endotoxin.

R Pfam; PF00555; Endotoxin.

R Pfam; PF00555; Endotoxin.

R Sporulation; Toxin.

VARIANT

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SEQUENCE 1228 AA; 139647 NW; C8E3A19FB5D98575 CRC64;
                                                                                                                                                                    Query Match 60.1
Best Local Similarity 62.4
Matches 447; Conservative
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Search completed: October 28, 2004, 18:29:54 Job time : 101.579 secs

P06578 bacillus th Q7be98 bacillus th Q9f296 bacillus th Aan76494 bacillus Aao13302 bacillus Aao13302 bacillus Q60407 bacillus th Q78xE9 bacillus th Q78xE9 bacillus th Q6eix3 bacillus th Q6eix3 bacillus th Q693t21 bacillus th Aas93798 bacillus th Q693t36 bacillus th

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STRAIN=JHCC4835; PubMed=1588820; MEDLINE=92269582; PubMed=1588820; Tailor R., Tippett J., Gibb G., Pells S., Pike D., Jordan L., Ely S.; "Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."; Mol. Microbiol. 6:1211-1217(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DSIR732; MEDLINE=92298009; PubMed=8517758; Gleave A.P., Williams R., Hedges R.J.; Gleave A.P., Williams R., Hedges R.J.; Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp.
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Q45752; P71092; Q45750; Q45751; Q45756;
30-MAY-2000 (Rel. 39. Created)
-30-MAY-2000 (Rel. 39. Last annotation update)
05-JUL-2004 (Rel. 44. Last annotation update)
Pesticidial crystal protein crylla (Insecticidal delta-endotoxin Cryll(a)) (Crystaline entomocidal protoxin (81 kba crystal protein). Name-crylla; Synonyms-cryll(a), cryV, cryV, CGCryV, Bacillus thuringlensis (subsp. kurstaki).

Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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STAIN-ABB8;
MDDLINE-56178985; PubMed=8606196;
Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V., Craig J.A., Koziel M.G., Estruch J.J.;
"Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=953[4293; PubMed=7793960; Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Ubstribution of cryv-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryv-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl. Environ. Microbiol. 59:1683-1687(1993).
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C1AB_BACTK
Q7BE98
Q9F296
AAN76494
AAO13302
Q9AM83
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Q7WZT9
Q6EIX3
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Q6PYW7
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        uppl. Environ, Microbiol.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=61;
  NCBI_TaxID=29339;
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                                                                                                     VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                              ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                                                                                                                                                                                                   TCTFCDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                                                                                                                              541 İGİFGDİRVNINPPFAQRYRVRİRYASİTDLOFHISINGKAINQGNFSAIMARGEDLDYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 TALFTSTNPRGLKTDVXDYHIDQVSNLVBSLSDBFYLDBKRELFEIVKYAKQLHIERNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Espindola N., Lemos M.V.F., Lemos B.G.M., Sena J.A.D.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY262167; AAP86782.1; -. InterPro; IPR001178; Endotoxin. InterPro; IPR005638; endotoxin. C. InterPro; IPR005639; endotoxin. C. InterPro; IPR005639; endotoxin. C. InterPro; IPR008979; Gal bind like. Pfam; PF03944; Endotoxin. C; I. Ffam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; PF03945; Endotoxin. M; I. Pfam; Pf03945; Endotoxin. M; I. Pfam; Pf03945; Endotoxin. M; I. Pfam; Pf03945; Endotoxin. M; I. Pfam; Pf03945; Endotoxin. M; I. Pfam; Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; I. Pf03945; Endotoxin. M; II Pf03945; Endotoxin. 
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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Last sequence update)
Last annotation update)
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Q6X181;
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1) -> Y (in strain v...
A -> V (in strain AB88).
A -> V (in strain HD-1 and strain 61).
FRQ -> NE (in strain HD-1 and strain 61).
FRQ -> NE (in strain HD-1 and strain 61).
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-> Y (in strain JHCC4835 and strain HD-
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                 Selvapandiyan A., Bhatnagar R.K.;
"Isolation, clouing and expression of cryV gene.";
"Sibmitted-(GCT-1996)-to-the-EMBL/GenBank/DDBJ databases.
-I--FUNCTION: Promotes.colloidosmotic-lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.
Active on Plutella xylostella and Bombyx mori.
-I--SUNCOMBENTAL STAGE: The crytail protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                      the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3756; DB 1;
Pred. No. 1.1e-252;
); Mismatches 1;
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EMBL; X62821; CAA44633.1; --
EMBL; 156338; AAC5999.1; --
EMBL; 19391; AAB00958.1; --
EMBL; 19391; AB00058.1; --
FIR; 139915; 139815.
FIR; S23383; S25383.
HSSP; PO2965; 1CIY.
InterPro; IPR00179; Endotoxin.
InterPro; IPR00159; endotoxin.
InterPro; IPR008979; Gal. bind like.
Ffam, PF03944; Endotoxin.M; 1.
Pfam; PF03945; Endotoxin.M; 1.
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                                                                                   GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW
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SEQUENCE FROM N.A.
Song F., Zhang J., Gu A., Huang D., Li G.;
Song F., Zhang J., Gu A., Huang D., Li G.;
Song F., Zhang J., Gu A., Huang D., Li G.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR373207; AAK66742.1; -.
HSSP; P02965; ICIY.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0006952; P:pathogenesis; IEA.
GO; GO:0006952; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR008979; Gal.bind_like.
Fram; PF03944; Endotoxin.C; I.
Fram; PF03944; Endotoxin.M; I.
SEQUENCE 719 AA; B1225 MW; C629DF2C44827241 CRC64;
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19, Last sequence update)
26, Last annotation update)
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Name=crylla;
Bacillus thuringiensis.
Bacteria; Firmicutes; B
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                        GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHILDFLEQVTIYSLLSRWSNTQYMMW
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GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
                                                                                 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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AAPB6782;
02-MAR-2004 (TrEMBLrel. 27, Created)
1 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
1 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
2 Cry11.
S CRY11.
Bacillus thuringiensis.
Baccheria, Firmicutes; Bacillales; Bacillaceae; Bacillus; NCRI 17, Last Dacillaceae; Bacillus; NCRI 18, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19, Carbon 19
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Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
Complete sequence of cryl1 gene of isolate T01 328 from
thuringiensis from Cubatao (SP - Brazil) soil.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY262167; AAP86782.1;
SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFFS CRC64;
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                                                                               EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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C STRAIN=S101;

Zhong Q., Dong Q., Yuan M., Pang Y., Wang X.;

L Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; ARPGF9593, ARCZ6910:1;

EMBL; ARPGF6953, ICIX.

R GO; GO:0005102; F: receptor binding; IEA.

R GO; GO:000592; P:receptor binding; IEA.

R GO; GO:000592; P:receptor binding; IEA.

R GO; GO:0009405; P:receptor binding; IEA.

R InterPro; IPR00653; endotoxin.

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R InterPro; IPR00653; endotoxin.

R InterPro; IPR00653; endotoxin.

R InterPro; IPR008579; Gal_bind_like.

R Ffam; PF00555; Endotoxin.

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Plasmid large plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29339;
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                                                                                                                  1 MKLKNODKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                  1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIBLQNINHEDCLKMSEYENVBPFVSASII
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81230 MW; 42746D478359BBA7 CRC64;
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Last annotation update)
                                      99.7%; Score 3750; DB 2; 99.7%; Pred. No. 2.8e-252; ive 0; Mismatches 2;
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
Bacillus cereus group; Bacillus thuringiensis.
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CAC85964;
02-MAR-2004 (TYEMBLYEL, 27, C.
02-MAR-2004 (TYEMBLYEL, 27, L.
02-MAR-2004 (TYEMBLYEL, 27, L.
Delta-endotoxin, CRYLIA.
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Gaps

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16; Indels
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     novel crylla-type
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Q8KY61,
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cry.
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
"Cloning and study of the expression of a novel crylla-
Bacillus thuringiensis subsp. kurstaki.";
J. Appl. Microbiol. 95.23-28 (2003).
BEMBL, AJ31511; CAC65964.1; -.
SEQUENCE 719 AA; 81203 MW; 8676E5A6C25DAFE8 CRC64;
                                                                                                Ouery Match 99.7%; Score 3748; DB 2;
Best Local Similarity 99.6%; Pred. No. 3.8e-252;
Matches 716; Conservative 1; Mismatches 2;
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                              TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
                                                                                                                                       TPRTVGFTTPFSFSDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 660
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                                                                                            TERIVGETIPES FLDVQSTF11GAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
Cryli(b)) (Crystaline entomocidal protoxin) (81 kDa crystal protein)
Names-ryll(b), Synoxyms=cryll(b), cryv, cryv465;
Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of certain coleopteran and lepidopteran species.
Active on Plutella xylostella but not on Bombyx mori.

-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the spore coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJURE=95314293; PubMed=7793960; Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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92.8%; Pred. No. 5.4e-236;
cive 31; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                            719 AA
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Pfam; PF00555; Endotoxin_M;
Pfam; PF03945; Endotoxin_N;
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SEQUENCE 719 AA;
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SERAINE=2837662; PubMed=12957903;

A SONG F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J., Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J., Li G., Hang D.;

In Strains and Characterization of a movel cryll-type genes from Bacillus thuringiensis strains and characterization of a movel cryll-type gene.";

Appl. Environ. Microbiol. 69:5207-5211(2003).

R MSD; PRO2065; LIT.

R MSD; PRO2065; LIT.

R GO; GO:000592; F:receptor binding; IEA.

GO; GO:000592; F:receptor binding; IEA.

GO; GO:000592; P:receptor binding; IEA.

GO; GO:000592; P:receptor binding; IEA.

R InterPro; IPR001178; Endotoxin.

R InterPro; IPR005638; endotoxin.

R InterPro; IPR005638; endotoxin.

R Fam; PF0055; Endotoxin.

R Pfam; PF0055; Endotoxin.

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            Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                       Bacteria; Firmicutes, Bacillales, Bacillaceae; NCBI_TaxID=1428;
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            01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                           Name=cryll;
Bacillus thuringiensis.
Plasmid pBTC19;
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Best Local Similarity 89.7°
Matches 645; Conservative
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MISCELLANEOUS: Toxic
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Sporulation; Toxin.
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-1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae. Active on Plutella xylostella and on Bombyx mori.

-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                  TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                       RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                           EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
"Cloning of a new Bacillus thuringiensis crylI-type crystal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIID BACTU STANDARD, PRT, 719 AA.

GONDEL,
16-0CT-2001 (Rel. 40, Created)
16-0CT-2004 (Rel. 44, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylid (Insecticidal delta-endotoxin Crylid)) (Crystaline entomocidal protein Crylid))
Crylid)) (Crystaline entomocidal protein Crylid) (Bactivialine entomocidal protein Crylid)

Bacillus thuringiensis.
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the protein is located
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                                             SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 3393; DB 1; ]; Pred. No. 2e-227; 35; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                            EMBL; AF047579; AAD44366.1; -. HSSP; P02965; 1CIY. InterPro; IPP001178; Endotoxin. InterPro; IPP005638; endotoxin. C. InterPro; IPP005639; endotoxin. N. InterPro; IPR005639; endotoxin. N. InterPro; IPR0089979; endotoxin. N. InterPro; IPR008979; endotoxin. Cit. Pfam; PF03944; Endotoxin. Cit. Pfam; PF03955; Endotoxin. M; 1. Pfam; PF03955; Endotoxin. M; 1. Sporulation; Toxin.
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30-MAY-2000 (Rel. 39, Last sequence update)
65-UUL-2004 (Rel. 44, Last annotation update)
69-Sesticidial crystal protein crylBb (Insecticidal delta-endotoxin crylB(b)) (Crystaline entomocidal protein).
                                                                                                                                                                                                                            GGHRLESKPIGGALNTSTQGSTNTSINPVTLQFTSRDFYRTESWAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                                                                                                                                       481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                           241 TGLNNLRAINGOSWVRXNOPRKDIELMVLDLVRVFPSYDTLVYPIKTISQLTREVYIDAI
                                                                                         GTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW
                                                                                                                    GCHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                                            VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDELYLDEKRELFEIVKYAKQIHIERNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-crylBD; Synonyms-crylB(b), cryET5;
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NOBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the delta endotoxin family.
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         TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719
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                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllc (Insecticidal delta-endotoxin
Cryll(c)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
Name-cryllc; Synonyms=cryll(c);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C18 / Egypt;
Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epithelial cells of insects.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
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                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Interpro, IPR005638; endotoxin C.
Interpro, IPR005639; endotoxin N.
Interpro, IPR008979; Gal bind like.
Pfam; PF03944; Endotoxin C; I.
Pfam; PF00555; Endotoxin M; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
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HSSP; P02965; 1CIY.
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                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis.
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                                                         Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- DPUSELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                    the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7318382413529F21 CRC64;
   Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.0%; Score 2445.5; DB 1;
65.6%; Pred. No. 4.2e-161;
iive 92; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001178; Endotoxin.
Interpro; IPR05638; endotoxin_C.
Interpro; IPR005639; endotoxin_N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PF00555; Endotoxin_C; I.
Pfam; PF00555; Endotoxin_M; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140451 MW;
                                                                                                                                                                                                                                                                                                                                                              EMBL; Z46442; CAA86568.1; -. HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF03945; Endotoxin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 65.6
470; Conservative
   Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sporulation; Toxin.
                                           SEQUENCE FROM N.A.
                   NCBI_TaxID=1441;
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30-MAY_2000 (Rel. 39, Last sequence update)
05-UL_2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
CrylB(c)) (Crystaline enchoscidal protoxin) (140 kDa crystal protein)
Name=crylBc; Synonyms=crylB(c), crylBc;
Bacillus thuringiensis (subsp. morrisoni).
                                                                                                                                                                  Gaps
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                                                                                                                                     Length 1229;
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                                                                                                                                                               Indels
                                                                                                       A4C949DB675C3269
                                                                                                                                    DB 1;
                                                                                                                                  65.0%; Score 2445.5; DB 1;
65.6%; Pred. No. 4.2e-161;
ive 92; Mismatches 138;
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IPR005638; endotoxin_C.
IPR005639; endotoxin_N.
IPR008979; Gal_bind_like.
                                       Pfam, PF03944; Endocoxin_C, 1.
Pfam, PF00555; Endocoxin_M, 1.
Span, PF03945; Endocoxin_N, 1.
Sportlation; Toxin.
SEQUENCE 1229 AA; 139769 MW;
                                                                                                                                                 Best Local Similarity 65.6
Matches 470; Conservative
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                            InterPro;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMAWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brizzard B.L., Whiteley H.R.; "In additional crystal protein gene cloned from "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis."; Nucleic Adds Res. 16:2723-2723 (1988).
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                                                                                                                                                                                                                                                                       596 RRAFTTPFTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIFVTATFEAEYDLERAQEAVNAL
                                                                                                                                                                        C1BA_BACTK STANDARD; PRT; 1228 AA.
PPOS57; 045731;
01-NOV-1988 (Rel. 09, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-7UL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylla (Insecticidal delta-endotoxin CrylB(a)) (Crystaline entomocidal protoxin) (140 kDa crystal protein)
                                                                                                                                               THP----IASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH
                                                                                                                                                                                                                                           VKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGT
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the spore coat.
                                                                            Name-crylBa; Synonyms-crylB(a), cryA4, Bacillus thuringiensis (subsp. kurstaki), and Bacillus thuringiensis (subsp. kurstaki), and Bacillus thuringiensis (subsp. entomocidus). Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=29339, 1436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the delta endotoxin family.
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SEQUENCE FROM N.A., STRAIN-HD-2, SPECIES-B.L.kurstaki, STRAIN-HD-2, MEDLINE-88203216, PubMed-3352680;
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SEQUENCE FROM N.A.
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                                                                               TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
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Pred. No. 2.1e-149;
0; Mismatches 162; Indels 25;
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Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF363025; ARK51084.1; --
HSSP; P07130; 1DLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis (subsp. entomocidus).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Delta-endotoxin CrylBa2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01130; IDLC.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0006952; F:defense response; IEA.
GO; GO:0009405; P:pathogeneais; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.
InterPro; IPR005639; Gal.bind_like.
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62.7%;
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Best Local Similarity
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LGTLGVPFAGQVASLYSFILGELWPXGKNQWEIFMEHVEEIINQXISTYARNKALTDLKG 130
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                                                                                                                                                                                         Query Match 60.5%; Score 2276.5; DB 1; Length 1228; Best Local Similarity 62.7%; Pred. No. 2.5e-149; Matches 449; Conservative 80; Mismatches 162; Indels 25;
                                                                                                                                               150 150 Y -> H (in strain HD-110).
1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;
                       InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal bind Ii)
Pfam; PR03844; Endotoxin.C; I
Pfam; PR0355; Endotoxin.M; I.
Pfam; PR03945; Endotoxin.N; I.
                                                                                                                                 Sporulation; Toxin.
VARIANT 150
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Search completed: October 28, 2004, 18:30:02 Job time : 106.579 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                             OM protein - protein search, using sw model
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October 28, 2004, 18:05:43 ; Search time 19.191 Seconds (without alignments) 3604.811 Million cell updates/sec US-10-019-823B-57 3760 1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYAKQLHIERNM 719 Run on:

Title: Perfect score: Sequence: Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 79:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

		d			SUMMARIES	
Result		Query	. '			
. L	Score	Match	Length	BB !	ID	Description
1	75	6.66		N	981	insecticidal prote
7	3747	99.7	Н	7	S25383	oral crysta
m	73	99.4	н	7	139814	ത
4	351	93.5	H	~	δ	cryV465 protein -
ស	ė.		2	7	37	parasporal crystal
φ	8		α	7	ın	hypothetical prote
7	14	39.7	1157	н	S49247	parasporal crystal
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11	w	•	S	N	JD0002	arasporal c
12	SO		15	N	A29125	arasporal
13	458.	•	m	N	A22798	arasporal
14	57.	38.8	17	N		ч
15	451.		~	N	2	arasporal
16	144	•	15	N	2	arasporal
17	47.	٠	17	N	31	arasporal
18	447.	•	^	N	23	arasporal
19	447.	٠	18	N	5	arasporal
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21	1358	•	17	N	5	arasporal
22	135		m	N	94	arasporal
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1160	1165	655	1172	1160	1178	1177	652	629	652	649	618	1156	1136	934	1180
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σ.	r.	32.1	31.8		30.9	30.9		30.2		26.2	24.8		22.0		

## ALIGNMENTS

1	rotein cryv1 - Bacillus thuringiensis 110s thuringiensis 1996 #sequence_revision 19-Jul-1996 #1 29814  Microbiol61.,2402-2407,1995  ibution of cryvtype-insecticidal protein mber: 139814, MUID:95314293; PMID:7793 38814  iminary, translated from GB/EMBL/DDBJ 719 <res- 3739;="" 99.4%;="" crystal="" db_2;<="" gb:l36338;="" nces:="" nid:9540281;="" parasporal="" pidn:aac="" protein="" score="" th=""><th></th><th>Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQYTIYSLLSRWSHTQYMMW 360  Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQYTIYSLLSRWSHTQYMMW 360  Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420  Db 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420  361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420</th></res->		Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQYTIYSLLSRWSHTQYMMW 360  Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQYTIYSLLSRWSHTQYMMW 360  Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420  Db 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420  361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420
OY 421 VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480 Db 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  481 ASHVKALVYSWTHRSADRINTIEPNSITQIELVKAPNLSSGAAVVGPGFTGGDILRRIN 540 [	II Bacillus thuringiensis  III. parasporal crystal protein cryV  Asion 17-Apr-1993 #text_change 09-Jul-2004  G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  22 acterization of a novel Bacillus thuringiensis delta-end  192269582; PMID:1588820  I protein  Score 3747: DB 2: Length 719;	S S S S S S S S S S S S S S S S S S S	OY 301 GTVHPHPSFTSTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTOYNNNW 360 Db 301 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVRNPHLLDFLEQVITYSLLSRWSNTOYNNNW 360 QY 361 GGHKLEFRIIGGTLNISTQGSTNTSINPVTLFFTSRDVYRTESLAGLNLFLTQPVNGVPR 420 Db 361 GGHKLEFRIIGGTLNISTQGSTNTSINPVTLFFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

421 VDFHWKEVTHPIASDNFYYPGTVGIGTQLQDSENELPPEATGQPNYESYSRRLSHIGLIS 480 421 VDFHWKEVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSRRLSHIGLIS 480 421 VDFHWKVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSRRLSHIGLIS 480 624 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540 625 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540 626 621 TGTFGDIRVNINPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMRGEDLDYK 600 627 621 TGTFGDIRVNINPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMRGEDLDYK 600 628 621 TFRTVGFTTPRFSFLDVGSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV 660 629 661 TFRTVGFTTPRFSFLDVGSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV 660 640 TFRTVGFTTPRFSFLDVGSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV 660 641 TFRTVGFTTPRFSFLDVGSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKV 660 651 TALFTSTNFRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719	QY 421 UDFHWKFYTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  L 1
ERNM 719 1-2004	Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719  RESULT 5 300873 parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis N.Alternate names: parasporal crystal protein cryA4 C;Species: Bacillus thuringiensis subsp. thuringiensis C;Date: 07-08p1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accesion: S00873 R;Brizzard, B.L.; Whiteley, H.R.
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tomocidus. A;Reference number: I39814; MUID:95314293; PMID:7793960 A;Reference number: I39814; MUID:95314293; PMID:7793960 A;Reference number: I39814; MUID:95314293; PMID:7793960 A;Reference into into into into into into into into	Nucleic Acids Res. 16, 2723-2724, 1988 Ayritle: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t Ayreference number: 800873; MUID:88203216; PMID:3362680 A;Accession: 800873; MUID:88203216; PMID:3362680 A;Accession: 800873; MUID:88203216; PMID:3362680 A;Accession: 800873 A;Accession: 800873; MIPROT:P05517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:9580949; A;Gene: cryA4 A;Statt codon: TTG A;Constrain: A;Constrain protein
Gaps 0;	C'ognetiants, parabotat C.ystat process. C'reywords: delta-endotoxin Ouery Match Best Local Similarity 62.7%; Pred. No. 2e-151; Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;
1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI	23 TDSLKNETDIELQNINHEDCLKWSEYENVEPPVSASTIQTGIGLAGKI 70
1 OTGIGLAGKILGTLGGVFFAGGVASLYSFILGELWPKKNOWEIFMENDEETINOKLSTYA  61 OTGIGLAGKILGTLGVPFAGGIASLYSFILGELWFKGKSOWEIFMENDEETINOKLILTYA  121 RNKALTDLKGLGDALAVYHDSLESWYGNRNNTRARSVVKSOYIALELMFVQKLFSFAVSG	BFILGELWPKGKNOWEIEWEHVEEIINOKISTYARNKALTD   ::     :     :      SFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALAR SYRNYTRARŞYVKSQYIALELMFVQKLIPSFAVSGEEVPLLP
121 RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVQKLPSFAVSG  181 EEVPLLPTYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS	Db 122 LGDSFRAYQQSLEDWLENPDDARTRSVLYTQYIALELDFINAMPLFAIRNOEVPLLMYYA 181 Qy 191 QAANLHILILRDASIFGKEWGLSSSEISTFYNRQYERAGDYSDHCVKWYSTGLINNLRGTN 250
OY 241 ISLANLEGINAESWYKINOPREDENJALEPSITIOMIERYTIAALITEKYIDAL 300  241 IGLANLEGINAKSWVRYNOPREDMILLANLEPSITIOMIERYTIAGUTEEVYTIDAL 300  OY 301 GTVHPHPSFTSTTWYNNAPSFSALEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMM 360	QY 251 AESWVRYNQFREDMILMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310  242 AASWVRYNQFREDILGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 299  0V 311 STTWYNNNAPSFSATEAAVVRNDHILDFIROVTTYSII.SEWSNTOVMNWGGHKI.EFFTT 370
Db 301 GTVHPNQAFASTTWYNNAAFSFAIEAAVIRSPHILDFIEKVTIYSLLSRWSNTQYMANW 360 Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420 Db 361 GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR 420	300 SMRWYNNNAPSFSAIEAAAIRSPHLLDFLBFLBQLTIFSASSRWSNTRHMIYWRGHTIQSRPI 371 GGTLNISIQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFV

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YLDEKRELFEIVKYAKOLHIERNM 719
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B59cies: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: B42459
B;Chambers J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C. Bacceriol. 173, 3966-3976, 1991
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene facerence number: A42459; MUID:91286178; PMID:2061280
A;Steference number: A42459; MUID:91286178; PMID:2061280
A;Steference number: A42459; MUID:91286178; PMID:2061280
A;Steference number: A42459; MUID:91286178; PMID:2061280
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                                                                                          FGDIRVNINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFR
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                                                         VNVPVYSWTHRSADRTNTIGPNRITOIPMVKASELPPGGTTVVRGPGFTGGDILRRTNTGG
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             596 RRAFTTPFTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFSAEYDLERAQEAVNAL
---IASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH
                                                                                                                                      TVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTAL
                                                                                                                                                                                    FISTNPRGLKTDVKDYHIDQVSNLVBSLSDEFYLDEKRELFBIVKYAKQLHIBRNM 719
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A;Residues: 1-380 «CH»
A;Cross-references: UNIPROT:Q8KX61; UNIPROT:Q45740; GB:M63897
C;Superfamily: parasporal crystal protein
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.Pred. No. 8.8e-126;
8; Mismatches 9;
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RESULT

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Datasporal crystal protein cry9Cal (validated) - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIH
C;Species: Bacillus thuringiensis
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A59350; S49247
R;Lambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; Vc
Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiansis insecticidal crystal protein with a high activity again
A;Reference number: A59350, MUID:96141404; PMID:8572715
A;Reference number: A59350
A;Wolecule type: DAA
A;Residues: 1-1157 cLAA>
A;Residues: 1-1157 cLAA>
A;Residues: 1-1157 cLAA>
A;Residues: Comment: This parasporal crystal protein, active against corn borer and other insects, C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Superfamily: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 1157;
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
39.7%; Score 1494; DB 1; Sest Local Similarity 43.3%; Pred. No. 1.7e-96; Matches 322; Conservative 116; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 LKNETDIELONINHEDCLKMSEYENVEPFVSAS
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parasporal crystal protein - Bacillus thuringiensis (strain aizawai)
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: A26513
R;Ceda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
R;Ceda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
A;Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis s
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Accession: A26513
A;Besidues: 1-1155 coBp.
A;Residues: 1-1155 coBp.
C;Supertamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 NINHEDCLKMSEYENVE-PFVSASTIQTG----IGIAGKILGTLGVPFAGQVASLYS
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.1%; Score 1472; DB 2; Length 1
Best Local Similarity 44.4%; Pred. No. 6e-95;
Matches 315; Conservative 113; Mismatches 227; Indels
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c;Species: Bacillus thuringiensis
c;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: $32645
R;Lambert, B.
Ribmitted to the EMBL Data Library, April 1993
A;Reference number: $32645
A;Accession: $32645
A;Accession: S32645
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parasporal crystal protein crylFa3 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S32649
R;Lambert, B.
Submitted to the EMBL Data Library, April 1993
A;Accession: S32649
A;Accession: S32649
A;Status: preliminary
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Best Local Similarity 44.8%; Pred. No. 9.9e-95;
Matches 325; Conservative 103; Mismatches 202; Indels
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RESULT 11

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parasporal crystal protein crylAb3 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomocpathogenic crystal prot
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: A90025; A91560; A90955; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463; 1987
A;Title: Cloning and mucleotide sequencing of two insecticidal delta-endotoxin genes from
A;Reference number: A90025
A;Accession: A90025
A;Accession: A90025
A;Accession: A90025
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A;Accession: A90025
A;Accession: A90
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R;Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal protei
A;Reference number: A91560; MUID:8716356; PMID:3557124
A;Accession: A91560
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: CHA>
A;Cross.references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
B;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerck)
B;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerck)
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A;Reference number: A26461; MUID:87054026; PMID:3023091
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A; Residues: 1-1155 < WAB>
A; Residues: 1-1155 < WAB>
A; Cross-references: GB: M13898; NID: g142719; PIDN: AAA22330.1; PID: g142720
A; Experimental source: subsp. berliner
B; Chak, K.F.; Jen, J.C.
B; Chak, K.F.; Jen, J.C.
A; Chak, K.F.; Jen, J.C.
A; Chak, K.F.; Jen, J.C.
A; Chescription: Complete nucleotide sequence and expression in Escherichia coli of a cry; A; Reference number: S14555
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AjCross-references: GB:X04698; NID:g40284; PIDN:CRA28405.1; PID:g40255
AjExperimental source: strain berliner 1715
Cj.Comment: This toxin is lethal to.the larvae of lepidopterans and dipterans.
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A, Residues: 1-1155 <GEI>
A, Residues: 1-1155 <GEI>
A, Cross-references: GB-MIS-211; NID: g143123; PIDN: AAA22561.1; PID: g143124
A, Cross-references: GB-MIS-211; NID: g143123; PIDN: AAA22561.1; PID: g143124
A; Experimental source: subsp. kurstaki
B, R; Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
A, Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gachierence number: A909555; MUID: 86300092; PMID: 3743328
A, Accession: A90955
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larity 44.5%; Pred. No. 1.8e-94;
Conservative 112; Mismatches 226;
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C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
F,82-586/Product: toxic peptide #status predicted
F;82-300/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
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parasporal crystal protein - Bacillus thuringlensis
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parasporal crystal protein - Bacillus thuringlensis
c;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
R;Shibano, Y: Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Cene: 34, 243-251, 1988
R;Atitles Nuclecide sequence coding for the insecticidal fragment of the Bacillus thuring
A;Reference number: A22798; MUD:85232070; PMID:2989108
A;Reference number: A22798
A;Residues: 1-934 cSHI>
A;Residues: 1-934 cSHI>
A;Cross-references: UNIPROT:Q985V8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
C;Comment: The authors translated the codon ACA for residue 264 as Ser.
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                 286 GIEGS-IRSPHLMDILNSITIYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNA 344
                                                                                                                                                                                                                                                                                                                                                                                                  STOGSTNISINPVILPFISRDVYRTESLAGLNLFLIQPVNGVPRVDFHWKFVTHPIASDN 436
                                   KEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLM 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 FYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 LPSAVYRKSGT--VDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 FILGELWPKGKNQWEIFWEHVEEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : | : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                       345 APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG----TSSN
                                                                                                                                                        VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S
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                                                                                                                                                                                                                                                                          324 AIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNTQYMMM---WGGHKLEFRTIGGTLNI
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A29125
A29125
Barasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29125
B;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme Bio/Technology 5, 807-813, 1987
A;Title: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Status: not compared with conceptual translation
A;Molecule type: DNA
DPINPALREEMRIQENDMNSALITTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG 179
                                                                                                                                 376
                                                                                                                                                                                                                                                                                                                                                                               286 GIEGS-IRSPHLMDILNSITIYIDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 FYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489
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                                                                                                                                                                                                                   VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S 323
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                                                                                              KEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNGFRRDMTLM
                                                                                                                                                                                                                                                                                                                                           AIEAAVVRNPHILDFLEQVTIYSLLSR----WSNTQYMNM---WGGHKLEFRTIGGTLNI
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Best Local Similarity 44.5%; Pred. No. 1.9e-94;
Matches 316; Conservative 112; Mismatches 226;
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A, Cross-references: UNIPROT: 09F296; UNIPROT: 093T21
C, Superfamily: parasporal crystal protein
C, Keywords: delta-endocoxin
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180 QRWGFDAATHNSRYNDLTRLIGNYTDAAGTWHENSERDWARNDRRELTLT 239  268 VLDUVALPSSYDTQMYPIKTTAQLTREVYTDAIGTWHPPSFTSTTWYNNNAPSFSAIBA 327	RESULT 15 Datasporal crystal protein crylha - Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Species: Bacillus thuringiensis C;Date: 28-Aug-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 C;Date: 28-Aug-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 C;Date: 28-Aug-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 C;Date: 28-Aug-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 B;Riddsysuringian; V; Nakamura, A; Mori, H; Masaki, H; Jozumi, T. B;Judysuringian; V; Nakamura, A; Moris Diologia, H; Moris Diologia, C;Reference number: JGC219; MUID:94289859; PMID:764972 A;Rocession: JCC219; MUID:94289859; PMID:7764972 A;Rosidues: J-176 < UDA> A;Rosidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA> A;Rossidues: J-176 < UDA A;Rossidues: J-176 < UDA A;Rossidues: J-176 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < UDA A;Rossidues: J-177 < U
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Search completed: October 28, 2004, 18:31:55 Job time: 22.191 secs

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3549.224 Million cell updates/sec
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1 MKLKNQDKHQSFSSNAKVDK......KRELFBIVKXAKQLHIERNM 719
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| cgn2_6/ptodata/2/pubpaa/DCOT_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ý	16,	Sequence 17, Appl	133	ď	ď	ď	ď	4,	4	4	equence 4,	72	Sequence 28,	n Ni	o,	7		11	13	15	equence 17	equence 28	equence 4,	equence 8,	equence 10	equence 12	equence 2,	equence 8,	equence 24	ednence 6,	7,
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Oct 29 15:06:25 2004

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Length 719;

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                                                                                    GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW
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APPLICANT: Carcard,
APPLICANT: Hargiss, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Carr, Nicholas B.
APPLICANT: Carr, Brian
ITILE OF INVENTION: AXXI-014, A Delta-Endotoxin Gene and
ITILE OF INVENTION: Methods for Its Use
FILE REPERENCE: 045600/274143
CURRENT FILING DATE: 2004-02-20
CURRENT APPLICATION NUMBER: 60/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
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1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                        QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA
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| Publication No. US20040210964A1
| GENERAL INPORMATION: US20040210964A1
| APPLICANT: Garozzi, Nadine APPLICANT: Garozzi, Nadine APPLICANT: Bargiss, Tracy APPLICANT: Borgis, Michael G. APPLICANT: Carr, Brian TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use FINERENCE: 045600/27448
| TITLE OF INVENTION: Methods for 12000 CURRENT APPLICATION NUMBER: US/10/782,096
| CURRENT FILING DATE: 2003-02-19
| PRICR FILING DATE: 2003-02-20
| NUMBER OF SEQ ID NOS: 23
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 719
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US-10-782-096-10
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APPLICANT: Glimer, Mary J.
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                                                                                             Score 3756; DB 17;
Pred. No. 4.5e-308;
0; Mismatches 1;
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7
                                                                                                99.00
99.00
                                                                                                Query Match
Best Local Similarity 99.9
Matches 718; Conservative
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US-10-428-961-42
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Publication No. US20040210865A1

GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Acaziel, Michael G.
APPLICANT: Carri, Michael G.
APPLICANT: Carri, Brian
ITILE OF INVENTION: Methods B.
APPLICANT: Duck, Nicholas B.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
ITILE OF INVENTION: AXMI -007, A Delta-Endotoxin Gene and
ITILE OF INVENTION: Methods for Its Use
GURRENT APPLICATION NUMBER: US/10/782,570
GURRENT FILING DATE: 2004-02-19
PRIOR FILING DATE: 2003-02-0

NUMBER OF SEQ ID NOS: 17
SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 719
                               Indels
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       Pred. No. 4.5e-308;
                            Mismatches
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  186.66
                         718; Conservative
       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1228;
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 2277.5; DB 16; Lengt; Pred. No. 8.8e-183; 80; Mismatches 162; Indels
             APPLICANT: BOTTGETTON, Johan
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Joos, Hans
TITLE OF INVENTION: CRYSTAL PROTEINS
TITLE OF INVENTION: CRYSTAL PROTEINS
TITLE OF INVENTION: CRYSTAL PROTEINS
TITLE APPLICATION NUMBER: US/09/661,016
PRIOR APPLICATION NUMBER: US/09/661,016
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 1990-05-30
PRIOR FILING DATE: 1990-05-30
PRIOR FILING DATE: 1980-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PEACHTIN VET: 2.0
SOFTWARE: PEACHTIN VET: 2.0
SERIO ID NO 10
                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bacillus thuringiensis US-10-809-953-10
   Van Mellaert, Herman
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Best Local Similarity 62.7%;
Matches 449; Conservative 8
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                                                                                                                                                                                  ) NAME/KEY: misc_feature
) LOCATION: (200)..(200)
) OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amin
US-10-428-961-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNKALADLKGLGDALAVYHESLESWIENRNNTRTRSVVKSQYITLELMFVQSLPSFAVSG 171
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PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
LENGTH: 710
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US-10-809-953-10
S-20-809-953-10
Sequence 10, Application US/10809953
Publication No. US20040181825A1
GENERAL INFORMATION:
                                                                                                                               TYPE: PRT
ORGANISM: Bacillus thuringiensis
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Matches 664; Conservative
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GENERAL INVOCATION.

APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Glimer, Amy Ju
APPLICANT: Glimer, Amy Ju
APPLICANT: Glimer, Amy Ju
APPLICANT: Glimer, Amy Ju
APPLICANT: Glimer, Amy Ju
TITLE OF INVENTION: Lepidoperan-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Lepidoperan-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Lepidoperan-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: VONDERE: US/10/428,961
CURRENT APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTION NUMBER: 60/153,995
NUMBER OF SEQ ID NOS: 63
LENGTH: 1227
TYPER: PRI
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                                                                                                                                                            PHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNE
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                                                                                                                                    220 FYNROVERAGDYSDHCVKWYSTGLNNLRGINAESWVRYNOFRRDMTLMVLDLVALFPSYD
                                                                                                                                                                                                                                                                                                                                                                340 EQVTIYSLLSRWSNTQYMNMGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVY
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Publication No. US20030237111A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 423; Conserval
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556 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/05/988,462

FILING DATE: 20-No. US20030046726A1-2001

CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.2%; Score 2264.5; DB 10; Length
64.3%; Pred. No. 1.1e-181;
tive 78; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UNN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
FILING DATE: 04-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHON: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                   APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1207 amino acids
                                                                                                                                    Sequence 7, Application US/09988462 Publication No. US20030046726A1 GENERAL INFORMATION:
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Best Local Similarity 64.3*
Matches 442; Conservative
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                                                                                 RESULT 7
US-09-988-462-7
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; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23
   ; FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 ESRIIRGSLSTWTHGNTNTSINPVTLQFTSRDVYRTESFAGINILLTTPVNGVPWARFNW 421
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                                     Sequence 23, Application US/09826660

Fatent No. US20010026940A1

CENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

APPLICANT: Narva, Kenneth E.

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1

FULE REFERENCE: MA-714XC2D1

CURRENT APPLICATION NUMBER: US/09/826,660

CURRENT FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23

PRIOR PLICATION NUMBER: 60/065,215

PRIOR PLICATION NUMBER: 60/065,215

PRIOR FILING DATE: 1998-03-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Datentin Ver. 2.0
                                                                                                                                                       62 IAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEHLIRQQVTENTRDTAL
SSNAKVDKISTDSLKN-----ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIG
                                                                                                                     66 IAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYARNKAL
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TYPE: PRT ORGANISM: Artificial Sequence

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                                                                                13 SSNAKVDKISTDSLKN-----ETDIBLQNINHEDCLKMSEYENVEPFVSASTIQTGIG
                                                                                                       62 IAGRILGVLGVPFAGQIASFYSFLVGEL#PRGRDPWEIFLEHVEQLIRQQVTENTRDTAL
                                                                                                                                                                                                                                     126 TDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPL
                                                                                                                                                                                                                                                                                                                  186 LPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNN
                                                                                                                                                                                                                                                                                                                                    LRGINAESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAIGTVHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 BFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 ALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGDILRRINTGTFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 SMCLNFNNTSLQRYRVRVRYRASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606 GFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIBFVPVEVTYEAEYDFEKAQEKVTALFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 HPSFTSTTWYNNNAPSFSALEAAVVRNPHILDFLEQVTIYSLLSRWSNTQYMNMWGGHKL
                                         13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1186;
Query Match 57.8%; Score 2171.5; DB 9; Length Best Local Similarity 59.0%; Pred. No. 7.5e-174; Matches 421; Conservative 108; Mismatches 172; Indels
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LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEBVPLLPIYA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 GGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLF--LTQPVNGVPRVDFHWKFV 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 LGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEBIINQKISTYARNKALTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 SMNWYNNNAPSFSAIETAVIRSPHLLDFILEQLTIFSTSSRWSATRHMTWRGHTIQSRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 ONTFERGTANYSQP-YESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSRVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 LVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGTFGD
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APPLICANT: Vanneste, Stijn
APPLICANT: Van Rie, Jercen
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
FILE REPERENCE: NEWETSUG.
CURRENT APPLICATION NUMBER: US/10/614,524
CURRENT PILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
FROM A PARTIL OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF THE SEC OF T
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Best Local Similarity 59.5%; Pred. No. 4.7e-169;
Matches 424; Conservative 98; Mismatches 181;
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; ORGANISM: Bacillus thuringiensis
US-10-614-524-2
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US-09-826-660-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPVGISASGSQ-TAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTN 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEEVPLLPIYA 190
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59.5%; Pred. No. 4.7e-169;
ive 98; Mismatches 181;
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Publication No. US20040016020A1
GENERAL INFORMATION:
APPLICANT: Arnaut, Greta
APPLICANT: Damme, Nicole
APPLICANT: Damme, Nicole
APPLICANT: Mathieu, Eva
                       PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEC ID NOS: 63
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Bacillus thuringiensis
US-10-428-961-38
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US-10-614-524-2
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                                                                                                                                   APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCOI
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REFERENCE: 968821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-05-02
PRIOR PLICATION NUMBER: D2000-03-03
PRIOR PLICATION DATE: 2000-08-03
PRIOR PLILNG DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/JP01/06660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14; Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 48.1%; Pred. No. 4.3e-136;
Matches 362; Conservative 125; Mismatches 220; Indels
                                                                              ; Sequence 1, Application US/10089678; Publication No. US20030017967A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1167
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Nava, Kenneth B.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA.714XC2D1
CURRENT APPLICATION NUMBER: US/09/826, 660
CURRENT FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 09/178, 252
PRIOR APPLICATION NUMBER: 60/065, 215
PRIOR PILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 25
LENGTH: 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 51.4%; Score 1932.5; DB 9; Length 643; al Similarity 57.7%; Pred. No. 4.6e-154; 371; Conservative 100; Mismatches 159; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
Sequence 25, Application US/09826660 Patent No. US20010026940A1 GENERAL INFORMATION: APPLICANT: Cardineau, Guy A.
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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60 PETFISSSTIQTGIGIVGRILGALGVPFASQIASFYSFIVGQLWPSKSVDIWGEIMERVE 119
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                                                            538 -RINIGIF---GDIRVNIN-PPFAQRYRVRIRYASTIDLQFHTSINGKAINQGNFSATMN 592
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120 ELVDQKIEKYVKDXALAELKGLGNALDVYQQSLEDWLENRNDARTRSVVSNQFIALDLNF
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                                                                                                                                              593 RGEDLDYKTFRTVGFTTPFSFLDVQSTFT----IGAWNFSSGNEVYIDRIEFVPVEVT
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49.1%; Pred. No. 1.9e-131;
iive 98; Mismatches 230; Indels 57;
                                                                                                                                                                                                                                                                                                                               US-10-78-141-16

JS-20-16, Application US/10782141

JS-20-16, Application US/10782141

JEDNEAL INFORMATION:

JAPPLICANT: GARCAZI, Nadine

APPLICANT: Rargiss, Tracy

APPLICANT: Roziel, Michael G.

APPLICANT: Carr, Brian

JTTLE OF INVENTION: Methods En Its Use

FILE REFERENCE: 045600/274143

CURRENT APPLICATION NUMBER: US/10/782,141

CURRENT APPLICATION NUMBER: 60/448,632

PRIOR APPLICATION NUMBER: 60/448,632

PRIOR APPLICATION NUMBER: 60/448,632

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus thuringiensis
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641 FEVEYDLERAQK 652
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Best Local Similarity 49.13
Matches 371; Conservative
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APPLICANT: Chu, Chin-Rei

APPLICANT: Chu, Chin-Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECOZO1-1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 6
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  SSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNL
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                                                                                                       Sequence 6, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus thuringiensis
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US-10-428-961-6
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Best Local S:
Matches 346,
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Search completed: October 28, 2004, 18:41:07 Job time: 70.6795 secs

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RESULT 1

US-08-266-870A-8

US-08-266-870A-8

Sequence 8, Application US/08286870A

Patent No. 605505

GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TAILOR, RH
APPLICANT: TAILOR, RG

TITLE OF INVENTION: BACTERIAL GENES
NUMBER OP SEQUENCES:
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSHURY, MADISON & SUTRO, LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STREET: 10006-5918

COMPUTER READABLE FORM:
MEDIUM TYPE: RDPPC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BREED RICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-ANT-1999
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1999
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
RESERRENCE/POCKET NUMBER: 16,773
RESERRENCE/POCKET NUMBER: 170608/220720
TELECOMMUTATION: NUMBER: 16,773
RESERRENCE/POCKET NUMBER: 170608/220720
TELECOMMUTATION: NUMBER: 170608/220720
TELECOMMUTATION: NUMBER: 170608/220720
TELECOMMUTATION: NUMBER: 170608/220720
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US-09-179-252-25
PCT-US-91-02560-25
PCT-US-91-02560-30
US-07-847-280-30
US-07-841-650-2
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TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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): /CGTZ_6/ptodata/1/iaa/6A_COMB.pep:*
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gaps

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                                                                                                                    Length 710;
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                                                                                                                        DB 4;
                                                                                                                   Query Match
92.4%; Score 3472.5; DB 4;
Best Local Similarity 92.4%; Pred. No. 1.8e-302;
Matches 664; Conservative 15; Mismatches 31;
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              FEATURE:

NAME/KEY: misc feature

LOCATION: (200)...(200)

OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
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Patent No. 6663605
GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TALLOK, RH
APPLICANT: TIPERT, JM
APPLICANT: TIPERT, JM
TITLE OF INVENTION: BACTERIAL GENES
INTERE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ORGANISM: Bacillus thuringiensis
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US-08-286-870A-4
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APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Brimer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Wupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MCC201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT APPLICATION NUMBER: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SEQ ID NOS: 63
SEQ ID NO 42
LENGTH: 710
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Query Match 99.8%;
Best Local Similarity 99.7%;
Matches 717; Conservative
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US-09-661-322A-42
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                                        481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
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                                                                                                                                                                                                                                                                                                                     601 TERTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYE
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APPLICANT: Osman, Yehia A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Mala, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
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89.7%; Pred. No. 1.6e-293;
live 33; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: W. Murray Spruill (Alston & Bird, STREET: 3605 Glenwood Ave. Suite 310 CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
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ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5716
TELECOMMUNICATION INFORMATION:
TELEFAM: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 89.73
Matches 645; Conservative
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TYPE: amino acid
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                                                                                                         STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3394; DB 3;
Pred. No. 1.8e-295;
0; Mismatches 1;
ADDRESSEE: Intellectual Property Group of ADDRESSEE: FILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W.
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70608/220720
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CLASSIFICATION: 435 1994
REACH APPLICATION DATA:
APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1990
PRICH APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY AGENT INFORMATION:
NAME: PAUL N. KOKULIS
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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
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amino acid
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Matches 647; Conservative
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181 EEVPLLPIYAQAANLHILLIRDASIPEKNGGLSASEISTFYNRQVERTRDVSYHCVKWAN 240 241 TGLNNLRGTNAESWVRYNQFREDMTLMVLDLVALFPSYDTGWYPIKTTAQLTREVYTDAI 300 241 TGLNNLRATNGGSWVRYNQFREDMTLMVLDLVALFPSYDTGWYPIKTTAQLTREVYTDAI 300 301 GTVPHPHSPTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEGVTIVSLLSRWSNTGYMMW 360 301 GTVDPNQALRSTTWYNNNAPSFSAIEAAVTRSPHLLDFLEKVTIVSLLSRWSNTGYMMW 360 301 GTVDPNQALRSTTWYNNNAPSFSAIEAAVTRSPHLDFLEKVTIVSLLSRWSNTGYMMW 360 301 GTVDPNQALRSTTWYNNNAPSFSAIEAAVTRSPHLDFLEKVTIVSLLSRWSNTGYMMW 360 301 GTVDPNQALRSTTWYNNNAPSFSAIEAAVTRSPHTCPFLDFLEKVTIVSLLSRWSNTGYMMW 360 301 GTVDPNQALRSTTWYNNAPSFSAIEAAVTRSPHTCPFTSCAUNFILDFLEKYTISSLLSHWSNTGYMMW 360 301 GGHRLESRPIGGLANTSTQGSTWTSINPVTLQFTSRDYRTESMAGLNLFTTQPVNGVPR 420 421 VDFHWKFPTLPIASDDRYYPGYVGIGTQLQDSSNELPPETTGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPIASDDRYYYGYVGIGTQLQDSSNELPPETTGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPIASDDRYYYGYVGIGTQLQDSSNELPPETTGQPNYESYSHRLSHIGLIS 480 421 VDFHWKFPTLPIASDDRYYNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTK 540 421 VDFHWKFPTLPIASDDRYYNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTK 540 421 VDFHWKFPTLPIASDDRYYNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTK 540 421 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWRGEDLDYK 600 541 GSHVKALVYSWTHRSADRYTNIIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTK 540 541 TGTFGDIRVNINPPFAQRYRVRYSTRIGKAINGGAFGAVRGFGFTGGDILRRTK 560 601 TFRTVGFTTPFSFSDVQSTFTIGAWNFSSGNEVTIGRAFLFETVVFAKQLHIERNM 719 61 TALFTSTNFRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVVKYRKQLHIERNM 719 61 TALFTSTNFRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVVKYRKQLHIERNM 719	THE APPLICATION OSTARY SECTION OS 09218942  GHEN NO. 6232439  WEREL NO. 6232439  WEREL NO. 6232439  WEREL NO. 6232439  TILE OF INVENTION: Accivity  TILE OF INVENTION: Accivity  THE OF INVENTION: Accivity  THE OF INVENTION WINNER: US/09/218,942  WEREL RAPPLICATION NUMBER: 09/003,217  WEREL RAPPLICATION NUMBER: 09/003,217  ARLIER PRILING DATE: 1998-01-06  ARLIER PAPLICATION NUMBER: 09/003,217  ARLIER PRILING DATE: 1998-01-06  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 2  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE: PAREIT OF NOS: 3  OFWARE

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247 AESWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRINAPSGFA 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 STWFINNVAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYWVGHRLNFRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 GGTLNISTOGST-NTSINPVTLPFTSRDVYRTESLAGINLFLTOPVNGVPRVDFHWKFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 HPIASDNEYYPG-----YVGIGTQLQDSENELPPEATGOPNYESYSHRLSHIGLISAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGTLGVPFAGOVASLYSFILGELWPKGKNOWEIFMEHVEEIINQKISTYARNKALTDLKG
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 850 ID NO: 4:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 2445.5; DB 1; 65.6%; Pred. No. 6.2e-210; iive 92; Mismatches 138; 1
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      1229 amino acids
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hes 470; Conservative
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Sequence 4, Application US/08100709

Sequence 4, Application US/08100709

Patent No. 532687

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Yuping

APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: DOXIN GENES AND PROTEINS CRYETS

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EBVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                     1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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                                                                                                                                                                                                                                                                                                    74.5%; Score 2800; DB 3;
llarity 99.8%; Pred. No. 2.5e-242;
Conservative 0; Mismatches 1;
                                  REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEFRONE: (202) 861-3000
TELEFAX: (202) 82-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
ATTORNEY/AGENT INFORMATION: NAME: PAUL N. KOKULIS
                                                                                                                                                                                 : 535 amino acids
amino acid
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; MOLECULE TYPE: protein
US-08-286-870A-6
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 534; Conserv
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GENERAL INCERVATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yughing
APPLICANT: Tan, Yughing
APPLICANT: Jany, Christine S.
APPLICANT: Genzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYET4 AND CTYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESSEDE: Danitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
247 AESWLRYNQFRRDLILGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRTNAPSGFA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542
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                                                                                                                                         311 STTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWWGGHKLEFRTI
                                                                                                                                                                                                                                                                                                                                                                         367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 --INPQNIYERGATTYSQPYQGVGIQLFDSETERPETTERPNYESYSHRLSHIGLIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 HVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
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                                                                                                                                                                                                                                                                                                                     GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 HPIASDNPYYPG-----YVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS
                                                                                                                                                                                              307 STWFINNWAPSFSAIEAAIFRPPHILDFPEQLIIYSASSRWSSTQHMYWVGHRLWFRPI
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CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTHARE: Patentin Release #1.0, Vex
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-UN-1995
CLASSIFFICATION S14
PR.OR APPLICATION NUMBER: US 08/176,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/176,709
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"AMDITHER: IBM PC COMPATIBLE
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REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELEPHONE: 115-757-1590
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08474038 Patent No. 5679343
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Donovan: William P.

APPLICANT: Tan, Yuping APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

APPLICANT: APPLICANT: APPLICANT: APPLICANT: Jany, Christine S.

APPLICANT: APPLICANT: APPLICANT: Jose M.

APPLICANT: Tan, Yuping APPLICANT: Jose M.

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                                                                                                   660 LFTSTNPRRLKTDVTDYHIDQVSNAVACLSDEFCLDEKRELFEKVKYAKRLSDERNL 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Panitch Schwarze Jacobs & Nadel c/o A.S.
Nadel
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30.DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-UL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLF, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Matches 470; Conservative
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U.S.A.
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ADDRESSEE:
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ADDRESSEE: Nadel
STREET: 1601 Market S
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-779-046-4
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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Patent No. 5854053

GENERAL INDFMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        311 STTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMGGHKLEFRTI 370 307 STNWFNNNAPSFSAIBAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHRLNFRPI 366
                                                                                                                                                                                                                                               TEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYKTF 602
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                                                                                                                                                                                                              LGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTALARLEG 126
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                                                                                                                                                                                                                                                                                                                                                                     GGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT 429
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                                                                                                                                                            13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGIAGKI
                                                                                                                  Gaps
                                                                                                                 17;
                                                                                          Length
                                                                                          Query Match
Best Local Similarity 65.6%; Pred. No. 6.2e-210;
Matches 470; Conservative 92; Mismatches 138; Indels
; SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids

; TYPE: amino acid

TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-474-038-4
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US-08-779-046-4
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251 AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 LGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQCVTENTRNTAIARLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 GGTLAISTOGST-NTSINPVTLPFTSRDVYRTESLAGLALFLTQPVAGVPRVDFHWKFVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSGEBVPLLPIYA
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c/o A.S.
                                                                                                                                                               COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
Panitch Schwarze Jacobs & Nadel
                                             Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 081100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLF, Christopher
REGISTRATION NUMBER: 27633
REGISTRATION NUMBER: 7205-49
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
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366 429 482 480 542 540 602 662

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PAPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: B.t. P8158C2, Active Against Lepidopteran Pests, and Genes TITLE OF INVENTION: B.t. P8158C2, Active Against Lepidopteran Pests, and Genes TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
127 LGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186
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                                                              251 AESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFT
                                                                                                                                               GGTLNISTOGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVT
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                                                                                                                                                                                                                             367 GGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF----
                                                                                                                                                                                                                                                                                                                                                              430 HPIASDNFYYPG-----YVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                             483 HVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF
                                      QAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-UUNE-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/448,170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08448170 Patent No. 5723758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~wanter: IBM PC Compatible
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US-08-448-170-10
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APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Christine S.
APPLICANT: Ganzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                     541 TFGDIRLNINVPLSQRYRVRIRYASTTDLQFFTRINGTTVNIGNFSRTMNRGDNLEYRSF 600
                                                                                                    TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 602
                                                                             RIVGFITTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTA 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,340

FILING DATE: 24-JUN-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/100,709

FILING DATE: 29-JUL-1993

ATTONNEY/AGENT INFORMATION:

NAME: EGG1F, Christopher:

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 72634

TELEPHONICATION INFORMATION:

TELEPHONIS: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.0%; Score 2445.5; DB 2;
65.6%; Pred. No. 6.2e-210;
iive 92; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i 1601 Market Street, 36th Floor
Philadelphia
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08881340 Patent No. 5942658 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1229 amino acids
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Best Local Similarity 65.6%
Matches 470; Conservative
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543
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COMPUTER READBLE FORM:
COMPUTER: FIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800 Encoding Lepidopteran-Active PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION: 800
ATTONNEY/AGENT INPORMATION:
NAME: SANGARY, JAY M.
REGISTRATION WINBER: 39,355
REFERENCE/DOCKET NUMBER: 39,355
REJECTATION: NUMBER: 39,355
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REJECTATION NUMBER: 39,355
REJECTATION NUMBER: 39,355
REJECTATION NUMBER: 39,355
REJECTATION NUMBER: 39,355
REJECTAT NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Su
CITY: Gainesville
STATE: Florida
COUNTRY: USA 488 amino acids MOLECULE TYPE: peptide TYPE: amino acid
STRANDEDNESS: sing TITLE OF INVENTION: US-08-961-803-10 GTVHPHPSFTSTTWYNNNAPSFSALEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW 360 61 OTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTVA 120 181 EEVPLLPIYAQAANLHILLIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240 241 TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 300 292 GIVHPPSFISTIWYNNNAPSFSTIEAAVVRNPHLLDFLEQVIIYSLLSRWSNIQYMNW 351 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420 352 GGHKLEFRTIGGTLNTSTQGSTNTSINPVTLPFTSRDVVRTESLAGLNLFLTQPVNGVPR 411 VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480 52 QTGIGIVGKILGNLGVPFAGQVASLYSFILGELWPKGKSQWEIFWEHVEELINQKISTYA 111 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 232 IGINRIMGNNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 291 27 1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI Length 488; DB 1; 62.2%; Score 2340.5; DB 1 89.5%; Pred. No. 3.6e-201; ive 13; Mismatches 30; PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 102D.C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (904) 372-5800
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide Query Match
Best Local Similarity 89.5
Matches 445; Conservative US-08-448-170-10 361 421 301 121 셤 g g 8 ద õ d ઠ ŏ 8 .8 8

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121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180 181 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240 TGLNRLMGNNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI 291 360 GTVHPHPSFTSTTWYNNNAPSFSTIEAAVVRNPHLLDFLEQVIIYSLLSRWSNTQYMNW 351 241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW 61 OTGIGIAGKILGTIGVPFAGOVASLYSFILGELWPKGKNQWEIFWEHVBEIINQKISTYA 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI Gaps 6 Length 488; Indels Query Match 62.2%; Score 2340.5; DB 3; Best Local Similarity 89.5%; Pred. No. 3.6e-201; Matches 445; Conservative 13; Mismatches 30; 172 232 301 ò ò g g 8 à

US-08-961-803-10
Sequence 10, Application US/08961803
Fatent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cummings, David A.
APPLICANT: Stelman, Kenneth E.
APPLICANT: Stelman, Stelman, Stelman, Stelman, Stelman, Stelman, Stelman, Stelman, Stelman, Stelman, TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 471

ASHVKALVYSWTHRSAD 497

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                                                                                                                                        100 QWEIFMEHVEEIINQKISTYARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVK 159
                                                                                                                                                                                                                                             250 TRIYPINISAQLTREVYTDAIGAT--GVNWASMWYNNNAPSFSAIEAAAIRSPHLLDFL 307
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                                                                                                 69
                                                              EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKN 99
                                                                                    70 QWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLY
                                                                                                                                                                                                                     SQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIST
                                                                                                                                                                                                                                                                                                                                                                            280 IQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 FFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQ1QD1IRTS1QGLSGNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 633 VYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS
                                                                                                                                                                                                                                                                                               220 FYNROVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIESLAGLNLF -- LIQPVNGVPRVDFHWKFVTHP -- -- LASDNFYYPGYVGIGTQLQDS
                          Gaps
                        13;
    64.3%; Pred. No. 1e-193; ive 78; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           693 DEFYLDEKRELFEIVKYAKQLHIERNM 719
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Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
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Launis, Karen L.
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Dunder, Erik M.
Pace, Gary M.
Suttie, Janet L.
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Bowman, Cindy G.
Best Local Similarity 64.3
Matches 442; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Koziel,
APPLICANT: Dewis, K
APPLICANT: Lewis, K
APPLICANT: Warren,
APPLICANT: Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-459-448A-7
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APPLICANT:
APPLICANT:
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                    GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420
                                                                                               421 VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
                                                              411
                                                                                                                       412 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 471
                                                   352 GGHKLEFRTIGGTLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-18805/A/CGC 1577/CIP
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APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-007-1991
ATTORNAGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 3-18805/A/C
TELEPHONE: (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                   Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
                                                                                                                                                                         481 ASHVKALVYSWTHRSAD 497
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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US-07-951-715A-7
                                                                                                                                                                                                                                                                        RESULT 14
US-07-951-715A-7
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573 FHTGINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSFLDVQSTFTIGAMNFSSGNF 632
                     ENELPPEATGOPNYESYSHRISHIGLISASHVKALVYSWTHRSADRINTIEPNSITOIPL 512
                                                                                                                                                                                                                         513 VKAFNLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQ
                                                                                                                                                                 544 FFVSRGGITVMNFRFLRIMNSGDELKYGNFVRRAFITPFTFTQ1QDIIRTS1QGLSGNGE
                                                                                                                                                                                                       633 VYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 SQYIALELMFVQXLPSFAVSGEEVPLLPIYAQAANLHILLIRDASIFGKEWGLSSSEIST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 FYNROVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQVIIYSLLSRWSNTQYMNMGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVY 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRD
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 SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.2%; Score 2264.5; DB 2; Length
64.3%; Pred. No. 1e-193;
.ive 78; Mismatches 154; Indels
   TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENTITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005
CITY: Tarrytown STATE: New York
                                                                                                                                                                      ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-UNN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8582
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207
                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
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Best Local Similarity 64.3
Matches 442; Conservative
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MOLECULE TYPE: protein
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(first entry)
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(ZENE ) ZENECA LTD.
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Paecilomyces sp.
                                                                                                                                                                                                        WO200100841-A1
                                                                                                                                                                                                                                      29-JUN-1999;
23-DEC-1999;
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                                                                                                                                                                                                                                                               Griffin J,
Vincent JL,
                                                                                                                                                                                                                  04-JAN-2001
          RESULT 1
AAB66910
Aae38272 B. thurin
Aab66911 Insectici
Aae38275 B. thurin
Aae38275 B. thurin
Aae38273 B. thurin
Aae38271 B. thurin
Aab6690 Insectici
Aae38271 B. thurin
Aab66912 Insectici
Aae38276 B. thurin
Aab67013 B. thurin
Aab67013 B. thurin
Aab67020 B. thurin
Aab07003 Bacillus
Aau02091 Bacillus
Aau02093 Bacillus
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Aae36274 B. thurin
Aab66908 Insectici
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Aau02041
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                                                                  1 MKLKNODKHOSFSSNAKVDK......KRELFEIVKYAKQLHIERNM
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                     lotal number of hits satisfying chosen parameters:
                                                                                            2002273 seqs, 358729299 residues
                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                         protein search, using sw model
                                   October 28, 2004, 17:51:02
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AAB66909
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AAB66907
ADM74717
AAB66912
AAE36276
AAU02041
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AAU02095
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Gapop 10.0 , Gapext
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3760
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Maximum DB seq length: 200000000
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Match Length
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Aaw32259 Bacillus
Aaw47639 CryET5. 3
Aaw8 633 CryET5. 3
Aay30923 B. thuring
Aaw4322 Bacillus
Aab19947 Bacillus
Aav50955 Bacillus
Aav5095 Bacillus
Aav71990 Chimeric
Aaw4421 Bacillus
Aay11990 Chimeric
Aaw4421 Bacillus
Aay116796 Amino aci
Aau00420 B. thurin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant production.
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100.0%; Score 3760; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-290;
Matches 719; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insecticide, transgenic plant, insect-resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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AAV31990
AAW44321
AAB19950
AAU02046
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AAU00421
AAU00420
AAB84628
AAU02039
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polymucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiens; insecticidal crivity. The present sequence is sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYWNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA
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                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                       protein comprising an X-glycine motif as an active ingredient of a pesticide
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 3760; DB 6;
100.0%; Pred. No. 1.2e-290;
ive 0; Mismatches 0;
                                                                                                                               Claim 12; Page 50-53; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 719; Conservative
                                   WPI; 2003-175137/17.
                                                                       insecticidal
inus, useful
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                                                                         QTGIGIACKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
                                                                                                 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                   121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                                 EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVXWYS
                                                                                                                                                                                                                                                                                                     TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                           EEVPLLP1YAQAANLHLLLLRDAS1FGKEWGLSSSE1STFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                             GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMW
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                     MKLKOVQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASII
                                                                                                                                                                                                                                                                                                                           TPRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B. thuringiensis insecticidal crystal endotoxin (CRY) protein,
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TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM 719

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07-JUN-2001; 2001GB-00013900

30-MAY-2002;

(SYGN ) SYNGENTA

TFRTVGFTTPFSFLDVQSTFT1GAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV

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protein. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crylla2
                                                                                              421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                                                  ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                              TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                TPRIVGETIPESFLDVQSTFT1GAWNFSSGNEVYIDRIEFVPVEVTYEAEXDFEKAQEKV
GCHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                  VDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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terminus, useful as an active ingredient of a pesticide.
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Pred. No. 2.5e-290;
0; Mismatches 1;
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99.9%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE36272 standard; protein; 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA LTD.
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Best Local Similarity
Matches 718; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transpents plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Warner SAJ;
                                                                                                                                                                                                Insecticide; transgenic plant; insect-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mackay EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 55-57; 72pp; English.
                                                      standard; protein; 719 AA.
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                                                                                                                                                                                                                                                                                                                                                                           99GB-00015215
                                                                                                                                                                                                                                                                                                                                          23-JUN-2000; 2000WO-GB002457
                                                                                                                                                              protein crylla2
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlile AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffin J, Carlile
Vincent JL, Lee MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-123015/13.
                                                                                                                                                                                                                                                                                                                                                                                                                              (ZENE ) ZENECA LTD.
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Matches 718; Conserv
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                                                                                                                                                                                                                                  Paecilomyces sp.
                                                                                                                                                                                                                                                                      WO200100841-A1.
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23-DEC-1999;
                                                                                                                                                              Insecticidal
                                                                                                                            12-APR-2001
                                                                                                                                                                                                                                                                                                        04-JAN-2001
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                                                    AAB66908
                                                                                        AAB66908;
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New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is B. thuringiensis (Bt) crystal protein Crylla, the DNA encoding which was mutated to allow cloning of domain II or domains I and II, to make the hybrid protexins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects
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Pred. No. 1.3e-289;
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Best Local Similarity 99.7%;
Matches 717; Conservative
                                  99EP-00203723
                                                                    99EP-00203723
                                                                                                                                          Bosch HJ;
                                                                                                                                                                          WPI; 2001-337141/36.
N-PSDB; AAS04855.
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                                     MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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/label= Signal_peptide
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                                                                                                                                                                                            VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSBNBLPPBATGQPNYESYSHRLSHIGLIS
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 B. thuringiensis insecticidal

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99.4%; Pred. No. 1.9e-289;
ive 2; Mismatches 2;
                                                                                                                                                                                                                                                                            Insecticide; transgenic plant; insect-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mackay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   РЈ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 62-64; 72pp; English.
                                                                                                                                                        719
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                                                                                                                                                                                                                                                                                                                                                                                                                          99GB-00015215.
                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000; 2000WO-GB002457
                                                                                                                                                          protein;
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Lee MD;
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                                                                                                                                                          AAB66911 standard;
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les 715; Conserv
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                                                                                                                                                                                                                                                                                                        Paecilomyces sp
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Vincent JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKALTDIKGIGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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                                                                                                                                                                                                                    Novel insecticidal protein obtained from species of Paecilomyces controlling insects, and for insect-resistant transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                            Score 3739; DB 4;
Pred. No. 5.7e-289;
L; Mismatches 3;
                                                                                                                                                   Mackay EA,
                                                                                                                                                   Cayley PJ,
                                                                                                                                                                                                                                                                            Claim 14; Page 57-59; 72pp; English
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                                                       23-JUN-2000; 2000WO-GB002457
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Best Local Similarity 99.4'
Matches 715; Conservative
                                                                                                                                                   Carlile AJ,
                                                                                                                                                                  Lee MD
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                                                                                                                      (ZENE ) ZENECA LTD
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  WO200100841-A1
                                                                                 29-JUN-1999;
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Vincent JL,
                              04-JAN-2001
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other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. 'sequence is used in the invention
                                                                                                                                                      MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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                                                                                 Score 3745; DB 6;
Pred. No. 1.9e-289;
3; Mismatches 2;
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Best Local Similarity 99.4%;
Matches 715; Conservative
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                                                                       GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW
                                                                                                                                                                                                                                GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera
                                              TGLNNLRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKITAQLIREVYIDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on pJH12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crystal; insecticide; toxin; delta endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tippett JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis; JHCC 4353 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR08041 standard; protein; 719 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Fig 5-10; 66pp; English.
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(first entry)
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25-MAR-2003
27-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is sequence is used in the invention
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                                                                                                                                            TALFISTNPRGIKTDVKDYHIDQVSNLVESISDBFYLDBKRELFEIVKYANBLHIBRNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                         thuringiensis insecticidal crystal endotoxin (CRY) protein, crylla3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTGIGIAGKILGTLGVPFAGQVASLYSFILGBLWPKGKNQWEIFMEHVEEIINQKISTYA
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                             TPRTVGFTTPFSFLDVQSTFT1GAWNFSSGNEVY1DR1EFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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                                                                  TFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIBFVPVBVTYBAEYDFBKAQEKV
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                                                                                                                    TALFTSTNPRGLKTDVKDYHIDQVSNLVBSLSDBFYLDBKRELFEIVKYAKQLHIBRNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New insecticidal protein comprising an X-glycine motif at terminus, useful as an active ingredient of a pesticide.
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Pred. No. 5.7e-289;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 47-50; 67pp; English.
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                                                                                                                                                                                                                                                                                 AAE36273 standard; protein; 719
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Best Local Similarity 99.4
Matches 715; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis.
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be used to produce transformants E.coli strain MCi2022/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-WAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TERTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVDVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                       QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
                                                                                                                                                                                                                                                                                                                 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSOYIALELMFVOKLPSFAVSG
                                                                                                                                                                                                                                                                                                                                   RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                                                                                                                                                         EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                   EEVPLL PIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSYHCVKWYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTVHPHPSFTSTTWYNNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                   Length 719;
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                                                                                                                                   Score 3735; DB 2;
Pred. No. 1.2e-288;
; Mismatches 4;
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Best Local Similarity 99.4%;
Matches 715; Conservative
                                                                                                        719 AA;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polymucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringienes, insecticidal activity. The present sequence is sequence is used in the invention

the amino-

at

New insecticidal protein comprising an X-glycine motif  $\varepsilon$  terminus, useful as an active ingredient of a pesticide.

30-MAY-2002; 2002WO-GB002666 07-JUN-2001; 2001GB-00013900.

SYGN ) SYNGENTA LTD

WPI; 2003-175137/17.

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Vincent

Bacillus thuringiensis.

WO200298911-A2 12-DEC-2002 Claim 12; Page 42-44; 67pp; English

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Gaps

1; 718;

Length Indels

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Sequence 718 AA;

9 9 120 120 180 180 240 240 360

360 420 419 480 479 539

ASHVKALVYSWTHRSADRTWTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN

480 481

CRY.

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B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryllal

26-JUN-2003

AAE36271

AAE36271

Insecticidal protein; pesticide; insecticidal crystal endotoxin;

ASHVKALVYSWIHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN

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121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                  BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                                                           QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
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                                                                                                       MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
     Score 3724.5; DB 6;
Pred. No. 8.2e-288;
); Mismatches 3;
                                     ·,
        99.1%;
Query Match
Best Local Similarity 99.4'
Matches 715; Conservative
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Bacillus thuringiensis cryl gene, expression vector, nucleotide sequence with high-toxicity to lepidoptera pests, encoded protein, primer sequences and the shuttle vector pSXX422b, useful as a pesticide.
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N-PSDB; ADM74716.
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 TGTFGDIRVNINPPFAORYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK
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                                                                                                                       TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM
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larity 99.3%; Pred. No. 2.5e-287;
Conservative 0; Mismatches 4; I
                                                                                                                                                                                                                                                                                                                                                              Insecticide; transgenic plant; insect-resistance
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99GB-00030536.
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Lee MD;
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23-DEC-1999;
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Vincent JL,
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Matches
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a 8 insect-resistance

Insecticide; transgenic plant;

WO200100841-A1 Paecilomyces

Insecticidal protein

15:06:25 2004

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           The invention relates to a novel Bacillus thuringiensis cryl gene, gene combination, expression vector, nucleotide sequence of the B thuringiensis cryl gene with high-texicity to lepidoptera pests and the amino acid sequence of the protein encoded by it, cooperative use of the cryl gene with the expression product of crylab or crylBa, primer sequences for expressing the genes, and the constructed shuttle vector pSX422b. The gene in combination with the crylab or crylBa genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the cryllel protein.
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                                                                                                                                                                                                                                                                                  MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNINHEDFLRMSEHESIDFFVSASTI
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                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB6613). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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Pred. No. 3.5e-271;
.; Mismatches 21;
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92.8%; Pre
cive 31;
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                                                                                                                                                        99GB-00015215.
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Best Local Similarity
Matches 647. Concom-
                                                                                                                                                                                              (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 719 AA;
                                                                                                                                                         29-JUN-1999;
                                                                                                                                                                     23-DEC-1999;
                                                                                                          04-JAN-2001
                                                                                                                                                                                                                   Griffin J,
Vincent JL,
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crivity. The present sequence is sequence is used in the invention
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             ASHVKALVYSWTHRSADRINTIEPNSIIQIPLVKAFNLSSGAAVVRGPGFIGGDILRRIN
                                                                                 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK
                                                            TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                                        TPRIVGETTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                                                                                                                                         Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
                                                                                                                                                                                                                                                                                                                                                                                         B. thuringiensis insecticidal crystal endotoxin (CRY) protein,
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92.8%; Pred. No. 3.5e-271;
ive 31; Mismatches 21;
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                                                                                                                                                                                                                                                                                                 AAE36276 standard; protein; 719
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis.
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Best Local Similarity
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                301 GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWW
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## ALIGNMENTS

RESULT 1 139814 insecticidal protein C; Species: Bacillus t C; Accession: 139814 R; Shin, B.S.; Park, Appl. Environ. Microl A; Title: Distribution A; Title: Distribution A; Reference number: 1 A; Accession: 139814 A; Stauus: preliminary A; Accession: 139814 A; Residues: 1-719 < RA A; Cross-references: C; Genetics: A; Gene: cryV1 C; Superfamily: parasp	Insecticidal protein cryV1 - Bacillus thuringiensis Insecticidal protein cryV1 - Bacillus thuringiensis C, pate: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999 C, Accession: 139814 R, Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I. Appl. Environ. Microbiol. 61, 2402-2407, 1995 A, Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis & A, Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis & A, Accession: 139814 A, Molecule type: DNA A, A, Coession: 139814 A, Molecule type: DNA A, Residues: 1-719 - RES A, Molecule type: DNA A, Residues: 1-719 - RES A, Gone: cryVI C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Genecics: C; Ge
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کن pp	61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEILFWHVDE-INOKISTY 119 
	120 ARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVS 179 
Oy Db	180 GEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSEISTFYNRQVERAGDYSDHCVKWY 239 
oy da	240 STGLANLRGTNAESWVRYNQFRRDMTLAVLDLVALFPSYDTOMYPIKTTAQLTREVYTDA 299 240 STGLNNLRGTNAESWVRYNQFRRDMTLAVLDLVALFPSYDTOMYPIKTTAQLTREVYTDA 299
o o	300 IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM 359 
λ <sub>O</sub>	360 WGGHKLEFRIIGGTLNISTOGSTNTSINPYTLPFTSRDVRTESLAGLNLFLTQPVNGVP 419 

Qy 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSBNELPPEATGQPNYESYSHRLSHIGLI 479	QY 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPBATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539	QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILKRT 539  480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILKRT 539
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWRRGEDLDY 599	QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDY 599
Qy 600 KTFRIVGFITPFSFLDVQSTFTIGAMNFSSGNEVYIDRIBFVPVEVTYEAEYDFBKAQBK 659	QY 6.00 KTPRTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPUEVTYBABYDFBKAQBK 659 (1)
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QY 420 RVDFHWKFYTHPIASDNFYYEGYAGIGTQLÖDSENELPPEATGQPNYESYSHRLSHIGLI 479 420 RVDFHWKFPTLPIASDNFYYLGYAGYGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI 479 420 RVDFHWKFPTLPIASDNFYYLGYAGYGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI 479 480 SASHVKALVYSWTHRSADFTNTIEPNSITQLPLVKAFNLSSGAAVYRGPGFTGGDILRRT 539 480 SASHVKALVYSWTHRSADFTNTIEPNSITQLPLVKAFNLSSGAAVYRGPGFTGGDILRRT 539 600 NTGFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWARGEDLDY 599 600 KTFRTVGFTTPPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVDVEVTYBAEYDFEKAQEK 659 600 KTFRTVGFTTPPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVDVEVTYBAEYDFEKAQEK 659 600 KTFRTTGFTTPPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVDVEVTYBAEYDFEKAQEK 659 600 KTFRTTGFTTPPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVDVEVTYBAEXDFEKAQEK 659 600 KTFRTTGFTTNPRGLKTDVKDYHIDQVSNLVESLSDEFFLEIVKYANGIHIERNM 719 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFFLEIVKYANGIHIERNM 719	RESULT 5  SUBSTANCE Crystal protein crysal - Bacillus thurisgiensis subsp. thuringiensis  Sparsporal crystal protein crysal protein crysal protein crystal protein crystal protein crystal protein crystal crystal protein crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal crystal cry
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C; Decies: Bacillus thuringiensis
C; Dete: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C; Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C; Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C; Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
B; Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.J.
Bacteriol. 173, 3966-3976, 1991
A; Title: Isolation and characterization of a novel insecticidal crystal protein gene facesion: B42459
B; By MulD: 91286178; PMID: 2061280
B; Betalianary
A; Molecule type: DMA
B; Besidues: 1-380 cHA>
A; Besidues: 1-380 cHA>
A; Cross-references: UNIPROT: Q8KY61; UNIPROT: Q45740; GB: M63897
C; Superfamily: parasporal crystal protein
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                                                                     LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711
1 MKLKNPDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKISEYENVEPFVSASTI
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9; Mismatches 9;
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RESULT

parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
N,Alternate names: parasporal crystal protein cryIH
C,Specias: Bacillus thuringiensis
C,Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004
C,Accession: A59350; A94247
Appl. Environ. Microbiol. 62, 80-86, 1996
A,Filte: A Bacillus thuringiensis insecticidal crystal protein with a high activity again A,Reference number: A59350; MUID:96141404; PMID:857215
A,Accession: A59350
A,Rolecule type: DN.AA
A,Residues: 1-1157 \*LAA
A,Residues: 1-1157 \*LAA
A,Residues: 1-1157 \*LAA
A,Cross-references: UNIPROT: Q45733; EMBL: 237527; NID:9547554; PIDN:CAA85764.1; PID:954755 A; Experimental source: serovar tolworthi C; Comment: This parasporal crystal protein, active against corn borer and other insects, C; Superfamily: parasporal crystal protein C; Keywords: delta-endotoxin 136 147 196 207 256 267 YNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYN 316 366 -----FRIIGGILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVP 419 468 520 580 QEDSYGLITTTRATINPGVDGTNR--İBSTAVDFRS-----ALIG-----IYĞVN 428 RVDFHWKFVTHPIASDNFYYPGYAGIGT-----QLQDSENELPP-EATGQPNYESY 469 634 648 694 78 707 88 79 AGQVASLYSFILGELWPKGKNQ-WEILFMEHVEE-INQKISTYARNKALTDLKGLGDALA 89 SGQIVSFYQFLLMTLWPVNDTAIWE-AFMRQVEELVNQQITEFARNQALARLQGLGDSFN 26 LKNETDIELQNINHEDCLKMSEYENVEPFVSAS-----TIQTGIGIAGKILGTLGVPF 29 LASDPNAALQNWWYKDYLQMTDEDYTDSYINPSLSISGRDAVQTALTVVGRILGALGVPF VYHDSLESWVGNRNNTRARSVVRSQYIAL5LMFVQKLPSFAVSGEEVPLLPIYAQAANLH LLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVR SHRLSHIGLIS------ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSS GITVLKGPGFTGGGILRRITNGFFGTLRVIVNSPLTQQYRLRVRFASTGNFSIRVLRGGV 649 IDRIEIVPUNPAREAEEDLEAAKKAVASLFTRTRD-GLQVNVTDYQVDQAANLVSCLSDE 469 THRISHVIPPSPOINQAGSIANAGSVPTYVWTRRDVDLNNTITPNRITOLPLVKASAPVS GAAVVRGPGFTGGDILRRTNTGTPGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGK IDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDE Gaps AINQGNFSATMNRGEDLDYKTFRTVGFTT-----PFSFLDVQSTFT1GAWNFSSGNEVY 92; Length 1157; NNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWS-NTQYMNMWGGHKLE Query Match
39.0%; Score 1466; DB 1; Length 1:
Best Local Similarity 43.2%; Pred. No. 7.3e-95;
Matches 322; Conservative 112; Mismatches 219; Indels FYLDEKRELFEIVKYANELHIERNM 719

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Ad5613

parasporal crystal protein - Bacillus thuringiensis (strain aizawai)

parasporal crystal protein - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004

C;Accession: A26513

R;Geda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamocto, H.; Nakayama, I.; Ohkawa, H.

R;Geda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamocto, H.; Nakayama, I.; Ohkawa, H.

R;Cene 53, 113-119, 1987

A;Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis s

A;Reference number: A26513

A;Reference number: A26513

A;Accession: A26513

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Best Local Similarity 44.1%; Pred. No. 9.8e-94;
Matches 313; Conservative 110; Mismatches 232; Indels 54
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parasporal crystal protein cryldal - Bacillus thuringiensis
c)species: Bacillus thuringiensis
c;becies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 832645
Filambert, B.
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A;Accession: 832645
A;Cacest-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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OYGHDKKMLLEAVRAAKRLSRERNL 732
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NyAlternate names: delta-endotoxin-2, entomocidal protoxin, entomopathogenic crystal protofyspecies: Bacillus thuringiansis
C;Species: Bacillus thuringiansis
C;Date: 28-Dec-1987 #sequence_response 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
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A; Reference number: A91560; MUD:87163505; PMID:3557124
A; Accession: A91560
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A; Accession: S14555

A; Residuae; DNA

A; Residuae: 1-115, CCHA-
A; Cross-references: EMBL: X54939; NID: g40272; PIDN: CAA38701.1; PID: g40273

R; Hoffe, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckh

R; Hoffe, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckh

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A; Hoffe, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckh

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A; Hoffer, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Jansens, S.; Mahillon, J.; Jansens, S.; Mahillon, J.; Jansens, S.; Mahillon, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, J.; Jansens, Jansens, Jansens, Jansens, Jansens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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Amesidues: 1-730,'L',732-784,'R',786-1155 <HOF>
Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
Experimental source: strain berliner 1715
Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
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A;Residues: 1-1155 <GEI>
A;Residues: 1-1155 <GEI>
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A;Experimental source: subsp. kurstaki
R;Wabiko, H:; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-1155 «WAB>
A,Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720
A,Experimental source: subsp. berliner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Title: Bacillus thuringiensis entomocidal protoxin gene sequence ;Reference number: A90955; MUID:86300092; PMID:3743328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1155;
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                                                           crystal protein cry1Ab3 - Bacillus thuringiensis
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llarity 44.2%; Pred. No. 3.1e-93;
Conservative 109; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Genericary 1-2; bt2
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
C;82-586/Product: toxic peptide #status predicted
F;82-300/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-1155 <KON>
A;Cross-references: UNIPROT:P06578
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Matches 314; Conserv
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parasporal crystal protein crylFa3 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 832649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 NINHE----DCLKMSEYENVEPFVSASTIQTGIGIA-GKILGTLGVPFAGQVASLYSFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELWPKGKNOWEILFMEHVEEINOKISTYARNKALTDLKGLGDALAVYHDSLESWVGNRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SSRNTAGNPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DSENELPPEATGQPNYESYSHRLSHI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.5%; Score 1449; DB 2; Length 1
44.5%; Pred. No. 1.2e-93;
tive 100; Mismatches 207; Indels
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RESULT 11

148 NRNNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLLRDASIFG 207

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paragonal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-7ul-1996 #sequence_revision 19-7ul-1996 #text_change 09-7ul-2004
C;Accession: 139838
M;Refford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
J. Biotechnol. 6, 307-322, 1887
A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki I
A;Reference number: 139838
A;Accession: 139838
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                 KEWGLSSSEISTFYNROVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNOFRRDMTLM 267
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                                           CRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPFAGQVASLYS
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                                                                                                                                                             ----LENFDGSFRGSAQ
                                                                                                                                                                                                        324 AIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNTQYMNM---WGGHKLEFRTIGGTLNI
                                                                                                                                                                                                                                            286 GIEGS-IRSPHLMDILNSITIYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNA
                                                                                                                                                                                                                                                                                                                                  : | : : : : : | : | | : | 345 APQQRIVAQLGGGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTBFAYG-----TSSN
                                                                                                                                                                                                                                                                                                                                                                                                  -SASHVKALVY
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                                                                                                                                                                                                                                                                                                      STQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDN
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38.1%; Score 1434; DB 2; Length 1

Best Local Similarity 44.1%; Pred. No. 1.3e-92;

Matches 313; Conservative 109; Mismatches 232; Indels
                                                                                                                                         240 VLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV-----
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A29125
A29126
Deparasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Accession: A29125
C;Accession: A29125
B;Orlochoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
B;Orlochoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
B;Orlochoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
B;Orlochoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
B;Orlochoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
B;Orlochoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
B;Orlochoff, D.A.; McCossion: A29125
A;Accession: A29125
A;Accession: A29125
A;Accession: A29125
A;Molecule type: DNA
A;Residues: 1-1156 AFIS-
A;Cross: references: UNIPROT:Q97296; UNIPROT:Q93721
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPINPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG 179
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DPINPALREEMRIQENDWNSALTTAIPLFAVQNXQVPLLSVYVQAANLHLSVLRDVSVFG 179
                                                                         KEWGLSSSEISTFYNROVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNOFRRDMTLM 267
                                                                                                     323
                                                                                                                                                                                                 AIEAAVVRNPHILIDFILEQVTIYSLISR----WSNTQYMNM---WGGHKLEFRTIGGTLNI 376
                                                                                                                                                                                                                                                                                                 GIEGS-IRSPHLMDILNSITIYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNA 344
                                                                                                                                                                                                                                                                                                                                                              377 STQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPRVDFHWKFVTHPIASDN 436
                                                                                                                                                                                                                                                                                                                                                                                             : | : : : : | : | | : | APQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTBFAYG-----TSSN 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 FYYPGYAGIGTOLODSENELPPEATGOPNYESYSHRISHIGLI-----SASHVKALVY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPSAVYRKSGT--VDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPFAGQVASLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLGLVD
                                                                                                                                                                     VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSF----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NINPPFAQRYRVRIRYASTIDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRIVGFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWITHRSADRINTIEPNSITOIPLVKAFNLSSGAAVVRGPGFIGGDILRRINTGIFGDIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGLKTDVTDYHIDQVSNLVECLSDEFCLDEKKELSEKVKHAKRLSDERNL 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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44.2%; Pred. No. 3.1e-93;
tive 109; Mismatches 231; Indels
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Matches 314;
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OY 268 VLDLVALPPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 327	Db 451 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDLIRRTSPGGISTL 510  Qy 548 RVNINPPFAQRYRRIRYASTTDLQFHTSINGKAINQGNFSATWRGEDLDXKTFRTVGF 607	RESULT 15 JO241 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7) parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7) N.Alternate names: 135K insecticidal protein C.Species: Bacillus thuringiensis C.Species: Bacillus thuringiensis C.Species: Bacillus thuringiensis C.Species: Bacillus thuringiensis C.Species: Bacillus thuringiensis A.Remarca Malber. J70241 A.Speric. Biol. Chem. 52, 1565-1573, 1988 A.Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein c. A.Reference number: J70241 A.Reference number: J70241 A.Reference number: J70241 A.Residues: J1176 S.MIT A.Residues: J1176 S.MIT A.Residues: J1176 S.MIT A.Residues: J1176 S.MIT A.Residues: J1177 S.MIT A.Residues: J1177 Comment: The 135K protein protein C.Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae. C.Superfamily: parasporal crystal protein C.Superfamily: parasporal crystal protein C.Keywords: delta-endotoxin	Query Match  Best Local Similarity  43.3%; Pred. No. 2.8e-92;  Matches 308; Conservative 115; Mismatches 228; Indels 61; Gaps 12;  Qy  36 NINHEDCLKMSEVENVE-PPVSASTIQTGIGIACKLIGTLGVPFAGOVASLYS 87  4 NFNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLISEF-VPGAGFVLGLVD 62  Qy  88 FILGELWPKGKNOWELLEWHYEEINQKISTYARNKALTDLKGLGBLAVYHDSLESKWVG 147  Db  63 ILMOIFGPSQWDAFLVOISQLINGRIEGGESNLYQIYABSERWEA 119  Qy  148 NRNNTARSVVRSQYIALELMFVQKLESFAVSGEEVPLLPIYAQAANLHLLLRABSIFG 207  150 DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVSVFG 179  Qy  208 KENGLSSSEISTFVNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDWTLM 267  180 QRWGFDAATINSRYNDLTRLIGNYTDYAVAWYSTGLNNLRGTNAESWVRYNQFREDTLT 239
Db 180 QRWGFDATINSRYNDLTRLIGNYTHAVDWYNTGLERVWGPDSRDWIRNDFRRELTLT 239  QY 268 VLDLVALFPSYDTQMYPIKTTAQLTREVYTDALGTVHPHPSFTSTTWYNNAPSFS 323  240 VLDIVALFPSYDTQMYPIKTTAQLTREVYTDALGTVHPHPSFTSTTWYNNAPSFS 323  QY 214 AIEAAVVRNPHLLDFLEQVITYSLLSRWANTQYMMWGGHKLEFRIGGTLNI 376  Db 286 GIEGS-IRSPHLMDILNSTITYTDAHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNA 344  QY 377 STQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFITQPVNGVPRVDFHWKFVTHPIASDN 436  Db 345 APQQRIVAQLGGGVXRTLSSTLYRRPPNIGINNQGLSVLDGTEFAYGTSSN 395  QY 437 FYYPGYAGITQLODSENBLPPRATGQPNYESYSHRLSHIGLISASHVKALVY 489  DD 396 LPSAVYRKSGTVDSLDEIPPQNNNVPPRQGFSHRLSHVGANSVSIIRAPMF 453	OY 490 SWITHSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGTFGDIRV 549	, ec H	Query Match  Best Local Similarity 43.3%; Pred. No. 1.7e-92;  Matches 308; Conservative 116; Mismatches 227; Indels 61; Gaps 12;  Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYS 87  bb 4 NPNINECIPPACHONELEFWEHVESINGKISTYPIDISLSITQFILSEF-VPGAGFYLGLVD 62  Qy 88 FILGELMPKGXNOWEILFWEHVESINGKISTYPIDISLSITQFILSEF-VPGAGFYLGLVD 62  Qy 148 NRNYTRARSVVRSQYIALELMFVQKLPFFANQAISRLEGLSNLYQIYAESFREWEA 119  Qy 148 NRNYTRARSVVRSQYIALELMFVQKLPFFANQAISRLEGLSNLYQIYAESFREWEA 119  Db 120 DPTNPALREEMRIQFNDKNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG 179  Qy 208 KEWGLSSSEISTFVNRQVERAGDYSDHCVKWYSTGLNNLRGINAESWVRXNQFRRDWILM 267  C) 180 QRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREITLT 239

δ	268 VLDLVALFPSYDTQMYPIXTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEA 327	
qq	ALFSNYDSRRYPI	
ζ	328 AVVRNPHLLDPLEQVTIYSLLSRWSNTQYMNWWGGHKLEFRTIGGTLNISTQGS 381	
qa	286 RIEQNIRQPHLMDILNSITIYIDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGN 340	
ò	382 INTSINPUTLPFTSRDVYRTSSLAGLNLFLTQPVNGVPRVDFHWKFVTHPI 432	
qu	341 AGNAAPPULVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTNL 397	
οχ	433 ASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASHVKAL 487	
qa	398 PSTIYRQRGTVDSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAP 450	
ò	488 VYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDI 547	
q <sub>0</sub>	451 TFSWQHRSAEFNNIPSSQITQIPLIKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTL 510	
λõ	548 RVNINPPFAQRYRVRIRYASTIDLQFHTSINGKAINQGNFSATWNRGEDLDYKTFRTVGF 607	
q	511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGF 570	
'n	608 TTPPSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEKVTALFTST 667	
q	SABYDLE	
ò	668 NPRGLKTDVKDYHIDQVSNLVBSLSDEFYLDEKRELFEIVKYANELHIERNM 719	
QC	631 NQIGLKTDVTDYHIDQVSNLVECLSDEKQELSEKVKHAKRLSDERNL 692	

Search completed: October 28, 2004, 18:31:57 Job time: 21.191 secs

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, MOLECULE TYPE: protein US-08-286-870A-8
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US-08-286-870A-8
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1 MKLKNQDKHQSFSSNAKVDK......KRELFEIVKYANELHIERNM 719
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Sequence 42,
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1: / GgTZ = 6/ptodata/1/iaa/5A_COMB.pep:*

2: / GgnZ = 6/ptodata/1/iaa/5B_COMB.pep:*

3: / cgnZ = 6/ptodata/1/iaa/6A_COMB.pep:*

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5: / cgnZ = 6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: / cgnZ = 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
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US-08-128-870A-6

US-08-179-046-4

US-08-179-046-4

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US-08-961-865-4

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US-09-178-252-25

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US-07-876-80-30

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US-07-812-80-30

US-07-812-80-30

US-07-812-80-30

US-07-812-80-30

US-08-315-468-2

US-08-315-468-2

US-08-315-468-2

US-08-315-468-2

US-08-315-847-5

US-08-325-547-5

US-08-3532-547-5

US-08-3532-547-5

US-08-3532-547-5

US-08-368-5

US-09-471-177-5

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US-08-962-1368-4
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## ALIGNMENTS

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APPLICANT: TALLOR, RH
APPLICANT: TALLOR, RH
APPLICANT: TALLOR, RH
APPLICANT: TALLOR, RH
APPLICANT: TALLOR, RH
APPLICANT: TIPETTY JW
APPLICANT: TIPETTY JW
APPLICANT: TIPETTY JW
APPLICANT: TIPETTY JW
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPENCE LUCHMAN DARBY & CUSHMAN
ADDRESSEE: ILTESIECTAIN FORDER, N.W.
CITT: WASHINGTON
STREET: 1100 New York Avenue, N.W.
CONDERSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 100 New York Avenue, N.W.
CONDUTRY: USA
ZIP: 20005-3918
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BARDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: 16,773
REPRENCED FORCET NUMBER: 16,773
REPRENCED FORCET NUMBER: 16,773
REPRENCED FORCET NUMBER: 16,773
REPRENCED FORCET NUMBER: 16,773
RELEPHONE: (202) 861-3000
TELEFOND FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENGWHYTION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
Sequence 8, Application US/08286870A Patent No. 6063605
GENERAL INFORMATION:
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TOPOLOGY: lim
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VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDEKRELFEIVKYAKQLHIERNM 710
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                                                                                                                                                               Indels
                                                                                                                             DB 4;
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; Pred. No. 3.3e-304;
16; Mismatches 31;
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CUSHMAN DARBY & CUSHMAN
                                    NAME/KEY: misc_feature
incartron: (200)...(200)
corner incommartion: No. 6593293-Coding
US-09-661-322A-42
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Patent No. 6054605
GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, UM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ORGANISM: Bacillus thuringiensis FEATURE:
                                                                                                                             91.5%;
91.9%;
                                                                                                                                                                 662; Conservative
                                                                                                                                              Similarity
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APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Bonovan, William P.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin C
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin C
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MCCO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
SEQ ID NO 42
LENGTH: 110
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                                                                                                        9
                                                                                                                                         OTGIGIAGKILGTLGVPPAGQVASLYSFILGELWPKGKNQWP/LFMEHVBB-INQKISTY
                                                                                               1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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                                                                          MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                       Gaps
                                       7
   Length 719;
                                      Indels
 DB 3;
                                      3; Mismatches
   Score 3720;
Pred. No. 0;
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Patent No. 6593293
GENERAL INFORMATION:
sch
11 Similarity 99.2%;
714; Conservative
 Query Match
Best Local Similarity
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US-09-661-322A-42
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                              540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY
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APPLICANT: Madkour, Magdy A.
APPLICANT: Madkour, Magdy A.
APPLICANT: Bulla, Lee A.
TITLE OF INVENTION: BROILLUS THURINGIENSIS ISOLATES WIT
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSED: W. Wurray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
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89.2%; Pred. No. 5.8e-295;
iive 35; Mismatches 41;
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US-009-003-217-2
Sequence 2, Application US/09003217
; Patent No. 5986177
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SPILIII, W. MILKERY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REFRENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 719 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy disk
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hes 642; Conservative
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COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,870A

FILING DATE: 05-AUG-1994

CLASSIFICATION NUMBER: US 07/52028

FILING DATE: 09-MAX-1990

PRIOR APPLICATION NUMBER: US 07/52028

FILING DATE: 09-MAX-1990

PRIOR APPLICATION NUMBER: US 08/52028

FILING DATE: 09-MAX-1990

PRIOR APPLICATION NUMBER: GB 8910624.9

FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:

NAME: PAUL N. KOKULIS

REFERENCE/DOCKET NUMBER: 70608/220720

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 4:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3370; DB 3;
Pred. No. 1.1e-297;
1; Mismatches 0;
ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.6%;
                                                                                                                                       ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity 99.5
Matches 646; Conservative
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CITY: Wa
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GENERAL INFORMATION:
APPLICANT: Osman, Yehia
TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
TITLE OF INVENTION: Activity
FILE REPERRINCE: Cry11
CURRENT APPLICATION NUMBER: US/09/218,942
CURRENT APPLICATION NUMBER: 60/035,361
EARLIER APPLICATION NUMBER: 09/003,217
EARLIER FILING DATE: 1998-01-06
EARLIER FILING DATE: 1998-01-06
SOFTWARE: PAPPLICATION NUMBER: 09/003,217
EARLIER FILING DATE: 1998-01-06
SOFTWARE: PAPPLICATION NUMBER: 09/003,217
EARLIER FILING DATE: 1998-01-06
SOFTWARE: PAPPLICATION NUMBER: 1998-01-06
SOFTWARE: PAPPLICATION NUMBER: 1998-01-06
SEQ ID NOS: 2
ELENTH: 719
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                                                                                                                  300 IGTVDPNQALRSTTWYNNNADSFSAIBAAVIRSPHLIDFLEKVTIYSLLSRWSNIQYMMM 359
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GEEVPLLPIYAQAANLHLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWN '239
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                                                  WGGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDFYRTESWAGLNLFLTQPVNGVP
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                                                                                               IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMM
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                                 STGINNIRGINAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDA
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US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Bacillus thuringiensis
US-09-218-942-2
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                                                                                                                                       300 IGTVDPNQALRSTTWYNNNAPSFSAIEAAVIRSPHILDFLEKVTIYSLLSRWSNTQYMNN
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                                                                                                                                                                                                            300 IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIXSLLSRWSNTQYMNM
                                                                                                                                                                                                                                                                                                                                             360 WGGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDFYRTESWAGLNLFLTQPVIGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTFRIVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                                                                                                                                                                                                                                                                                                               360 WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
                                                                                                                                                                                                                                                                                                                                                                                                                     420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 RVDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STGINNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATEM: PC-DOS/Ms-DOS
SOFTWARE: PATEM: PC-DOS/Ms-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :SEE: Intellectual Property Group
SEE: PILLSBURY, MADISON & SUTRO L.
: 1100 New York Avenue, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08286870A
Patent No. 6063605
GENERAL INFORMATION:
APPLICANT: ELY, S.
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
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310 TSTIWYNNNAPSFSAIEAAVVRNPHILDFLEQVIIYSLLSRWSNIQYMNWGGHKLEFRI 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 ASTWWFNNNADSFSAIEAAIFRPPHLLDFPEQLIIYSASSRWSSTQHMYWVGHRINFRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVPLLPIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAIGTVHPHPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 NAESWERYNOFRRDLTLGVLDLVALFPSYDTRTYPINTSAOLTREIYTDPIGRTNAPSGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%; Score 2417.5; DB 1; Length 1229; 65.3%; Pred. No. 1.6e-210; ive 90; Mismatches 140; Indels 19;
                                                                                    COMPUTER KAALADLE FUNDED

COMPUTER: ENDER PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27634
TELERPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1229 amino acids
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                                                    ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 46
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; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
    APPLICANT: Donovan, William P.
    APPLICANT: Tan, Yuping
    APPLICANT: Tan, Yuping
    APPLICANT: Gonzalez Jr., Jose M.
    TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
    TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
    NUMBER OF SEQUENCES:
    ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
    ADDRESSEE: Panitch Schwarze Jacobs & Nadel street, 36th Floor
    STREBT: 1601 Market Street, 36th Floor
    CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNOWEI-FMEHVEEIINOKISTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARNKALTDIKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDXSDHCVKWY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STGLNNIRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDA 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.8%; Score 2776; DB 3;
Best Local Similarity 99.4%; Pred. No. 9.5e-244;
Matches 533; Conservative 1; Mismatches 0;
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKTUIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPA: (202) 861-300
TELEPA: (302) 822-0944
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TOPEC: amino acids
                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                     JS-08-286-870A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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Sequence 4, Application US/08474038

Patent No. 5679343

GENERAL INFORMATION:
APPLICANT:
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Jany Christine S.
APPLICANT: Jose M.
APPLICANT: Jany Christine S.
APPLICANT: Jose M.
APPLICANT: Jany Christine S.
APPLICANT: Jany Christine S.
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 FRTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 ALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 NAESMLRYNQPRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRTNAPSGF
                                                                                                                                                                             306 ASTINMENNIAPSESAIEAAIFRPPHILDFPEQLTIYSASSRWSSTQHMNYWVGHRLNFRP
                                                                                                                                                                                                                                                         370 IGGILNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 NTLRAPVYSWTHRSADRINTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRTWT
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                                                                                                                                                                                                                                                                                                                                                                                                    429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA
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CITY: Philadelphia
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APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-UNM-1995
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/106,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7205-49
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennsylvania
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APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Generalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryet4 AND cryet5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                      130 GLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVPLLPIY
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Nadel
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CURRENT APPLICATION DATA:

PEDICATION NUMBER: US/08/176,865

FILING DATE: 30-DEC-1993

CLASSIFICATION: 435

PRICK APPLICATION DATA:

APPLICATION NUMBER: US 08/100,709

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: EGGLE, CATISTOPHER

REGISTRATION NUMBER: 2763

REFERENCE/DOCKET NUMBER: 2763

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08176865
Patent No. 5616319
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ADDRESSEE:
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Matches 469;
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Panitch Schwarze Jacobs & Nadel c/o A.S.
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APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: GGOLF, Christopher
REGISTRATION NUMBER: 27633
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity 65.3
469; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
              ADDRESSEE: Nadel
STREET: 1601 Market
CITY: Philadelphia
                                                           Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                         STATE: Pe
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Best Local S:
Matches 469,
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APPLICANT: Tan, Yubing
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
NUMBER OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      GLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVPLLPIY 189
                                                                                                                                                                                                                                                                                                AQAANLHLLLLRDASI FGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 ASTINWENNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVGHRINFRP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---INPONIYERGATTYSOPYOGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLIG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 IGGTLNISTQGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFV 428
                                                                                                                                                                                                                      LGTLGVPFAGQVASLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 IGGTLNTSTOGLTNNTSINPVTLOFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF--- 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKT 601
                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                    TSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLEFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNT
                                                                                                                                                              13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIGLAGKI
                                                                                                                                                                                        7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEVNNIDPFVSASTVQTGINIAGRI
                                                                                                                                   Gaps
                                                                                                                                  19;
                                                                                                     Length 1229
                                                                                                                                  Indels
                                                                                                    tch 64.3%; Score 2417.5; DB 1; sal Similarity 65.3%; Pred. No. 1.6e-210; 469; Conservative 90; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08779046 Patent No. 5854053 GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                         MOLECULE TYPE: protein US-08-474-038-4
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US-08-779-046-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                      COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/779,046 FILING DATE: 06-JAN-1997 CLASSIFCATION: 435 PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%; Score 2417.5; DB 2;
65.3%; Pred. No. 1.6e-210;
ive 90; Mismatches 140; ]
Street, 36th Floor
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Sequence 10, Application US/08448170

Patent No. 5723758
GENERAL INFORMATION:

APPLICANT: Cannon, Raymond J.C.

APPLICANT: Cannon, Raymond J.C.

APPLICANT: Stelman, Steve

TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted

TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: 10

ADDRESSEE: David R. Saliwanchik

ADDRESSEE: David R. Saliwanchik

ADDRESSEE: David R. Saliwanchik
                                                                                                                                            309
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                                                                                                                                                                                                                                                                                                                                     370 IGGILNISTOGST-NTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFV 428
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                                                                                                                                                                                    246 NAESWERYNOFRRDLILGVIDLVALFPSYDTRTYPINTSAOLTREIYTDPIGRINAPSGF
                                                                                                                                                                                                                                                                   306 ASTIWFINNADSFSAIEAAIFRPPHLLDFPEQLIIYSASSRWSSTQHMYWVGHRLNFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 AQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGT
                                                                            250 NAESWVRYNOFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVHPHPSF
                                                                                                                                                                                                                                       310 TSTTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLEFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNT
                                                                                                                                                                                                                                                                                                                                                                                 366 IGGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNF---
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STREET: 2421 N.W. 418t. Street, Suite A-1
CITY: Gainseville
STREE: Forida
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-UNB-1993
CLASSIFICATION: 424
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,170
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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US-08-448-170-10
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Patent No. 5942658

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Vuping

APPLICANT: Jany, Christine S.

APPLICANT: Gorzalez Jr., Jose M.

TITLE OF INVENTION: BACTLLUS THURINGIENSIS cryET4 AND cryET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel
                            130 GLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVPLLPIY 189
  GTPGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKT 601
                                                                                              FRIVGFITPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVT 661
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                                                                                                                                                                                                                        ALFISTNPRRIKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLSDERNL 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-UN-1997
CLASSIFICATION: 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-75-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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US-08-881-340-4
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52 ÓTGIGÍVGKILGNLGVPFAGQVASLYSFILGELWPKGKSQWEI-FWEHVEELINQKISTY 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 GEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 IGTVHPHPSFTSTTWYNNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM 350
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  Encoding Lepidopteran-Active Toxins
                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: BELLOATION NUMBER: US/08/961,803 FILING DATE: 31-0CT-1997 CLASSIFICATION: 800
                           STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                               PRICEASTITION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: US 08/448,170
PRICEA PEPLICATION NUMBER: US 08/448,170
FILING DATE: 23-WAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION: NAME: SANGERS, US WEGISTRATION NUMBER: 39,355
                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: M/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPRX: (352) 375-8100
TELEPRX: (352) 372-8600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 89.4
Matches 445; Conservative
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TITLE OF INVENTION: EN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                             Florida
: USA
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Patent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Renneth E.
APPLICANT: Narva, Renneth E.
APPLICANT: Steve
TITLE OF INVENTION: No. 6150889el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PSISSC2, Active Against Lepidopteran Pests, and Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 GEEVPLLPIYAQAANLHLLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKEYSDHCVKWY 230
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89.4%; Pred. No. 3.6e-202;
iive 13; Mismatches 29;
                                      FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAIJWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFREADION NUMBER: 31,794
REFREADION NUMBER: 31,794
REFREADION NUMBER: 31,794
REFREADION: (904) 375-8100
ITELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                         APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
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TYPE: amino acid
STRANDEDNESS: single
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    PRIOR APPLICATION DATA:
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US-08-961-803-10
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Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
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Lewis, Kelly S.
Kramer, Vance C.
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Launis, Karen L.
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APPLICANT: KOZIEL,
APPLICANT: Desai,
APPLICANT: Lewis,
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                   351 WGGHKLBFRTIGGTLNTSTQGSTNTSINPVTLPFTSRDVYRTBSLAGLNLFLTQPVNGVP 410
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WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419
                                                                         411 RVDFHWKFVTHPIASDNFYYPGYAGIGTOLODSENELPPEATGOPNYESYSHRLSHIGLI
                                                       RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                           Sequence 7, Application US/07951715A Patent No. 5625136
                                                                                                                                                                                                                                                                                                                                                                                             Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                                                             SASHVKALVYSWTHRSAD 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: TANGETH: 1207 amir-1707.
                                                                                                                                                                                                                                                    Koziel, Michael G.
Desai, Nalini M.
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Warren, Gregory W
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                                                                                                                                                                                                                                                                                                                          Evola, Stephen V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pace, Gary M.
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MOLECULE TYPE: protein
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New York
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                                                                                                                10 EDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLGVVFAGQLASFYSFLVGELWPRGRD
                                                                                                                                                                                                                                                                                            159 RSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIS
                                                                                                                                                                                                                                                                                                                           339 LEQVIIYSLLSRWSNTQYMNMWGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 LEQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 SENELPPEATGOPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITOIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 SETELPPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRTNTIGPNRITQIP
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                                                                              EDCLKMSEYENVEPFVSASTIQTGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKN
                                                                                                                                                                                                                                       70 QWEI-FLEHVEGLINGQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 DIOMYPIKTIAQLIREVYIDAIGTVHPHPSFISTIWYNNNAPSFSAIEAAVVRNPHLLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 DTRTYPINTSAQLTREVYTDAIGAT--GVNWASMWYNNAPSFSAIEAAAIRSPHLLDF
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                                                                                                                                                                                                                                                                                                                                                                                                    219 TPYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSY
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                              Gaps
                              15;
                            Indels
  64.1%; Pred. No. 4.7e-194;
ive 76; Mismatches 156;
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US-08-459-448A-7
'S Genero,' Application US/08459448A
'Patent No. 5859336
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Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
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Suttie, Janet
Best Local Similarity 64.19
Matches 441; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 TFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTQMYPIKTTAQLTREVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDF 338
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SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
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                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10591-9065
ZIP: 10591-9065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 40-0CT-1991
ATTORNEY/AGENT INPORMATION:
REFERENCY/DOCKET NUMBER: CG 1577/CIP/DIV4
TELEPHONE: (919) 541-8689
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
COUNTY. AND ADDIVERSELY SEQ OF THE SEGUENCE CHARACTERISTICS:
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                         TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94 CORRESPONDENCE S. 94 CORRESPONDENCE ADDRESSEE: No. 5559336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005 CITY: Tarrytown STREET: New York COUNTRY: USA
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   INVENTION:
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Best Local Similarity
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542
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                                                                                                                                                                                                                                                                                          691
                                                                                                                         632 EVYIDRIEFVPVEVTYBABYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESL
                                                                                                                                                                                                                                                                                                                       452 SENELPPEATGOPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRINTIEPNSITOIP
                                                                                               512 LVKAFNLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDL
                                                                                                                                                                                                                                                                                                                                                                                          692 SDEFYLDEKRELFEIVKYANELHIERNM 719
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Search completed: October 28, 2004, 18:34:21 Job time : 25:3343 secs

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P06578 bacillus th
Q7be98 bacillus th
Q96296 bacillus th
Aan76494 bacillus
Aao13302 bacillus
Q96483 bacillus th
Q69121 bacillus th
Q69721 bacillus th
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Aas93798 bacillus th
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Tounnisi S., Jaouai S.;
Tounnisi S., Jouari N., Jaoua S.;
Tounnisi S., Jouari N., Jaoua S.;
Tounnisi S., Jouari N., Jaoua S.;
Bacillus thuringiensis subsp. kurstaki.";
J. Appl. Mucrobiol. 95:13-28(2003).
BEMBL; AJ31512;
CAC855641.;
SEQUENCE 719 AA; 81203 MW; 8676E5A6C25DAPE8 CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                      MISCELLANEOUS: Toxic segment of the protein is located in the N-
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-> Y (in strain JHCC4835 and
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-!- SIMILARITY: Belongs to the delta endotoxin family.
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llarity 99.3%; Pred. No. 1.9e-252;
Conservative 2; Mismatches 1;
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InterPro; IPR008979; Gal_bind_like.
Edm, PP03944; Endotoxin_C; 1.
Pfan; PP00555; Endotoxin_M; 1.
Pfan; PP03945; Endotoxin_N; 1.
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InterPro; IPR005638; endotoxin
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EMBL; X62821; CAA4463.1; --
EMBL; L36338; AAC36999.1; --
EMBL; L49391; AAB00558.1; --
EMBL; X08920; CAA70124.1; --
EMBL; S25381; S25383;
HSSP; P02965; ICIY
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                                                    RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
                                                                                                                                                                              SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
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Q45752, P71092, Q45750, Q45751, Q45756;
Q45752, P71092, Q45750, Q45751, Q45756;
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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05-JUL-2004 (Rel. 47, Last annotation update)
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MEDLINE=91298009; PubMed=8517758;
Gleave A.P., Williams R., Hedges R.J.;
Gleave A.P., Williams R., Hedges R.J.;
screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes characterization of a cryV gene cloned from B. thuringiensis subsp.
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                              STGLINILRGTNAESWVRXNQFRRDMTLMVLDLVALFPSXDTQMYPIKTTAQLTREVYTDA
                                                                                                                                              IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM
                                                                                                                                                                                                                                       360 WGGHKLBFRTIGGTLNISTQGSTNISINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
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STGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDA
                                                                                                       IGTVHPHPSFTSTTWYNNNAPSFSAIBAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM
                                                                                                                                                                                                              WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
"Complete sequence of cryll gene of isolate T01 328 from thuringiensis from Cubatao (SP - Brazil) soil.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY262167; AAR95792.1; -- SEQUENCE 719 AA; 81216 WW; 3627E5A6C25DAFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRÝII.
Bacillus thuringiensis.
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
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Last sequence update)
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
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  IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM 359
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                                                  WGGHKLEFRIIGGILNISTQGSTNTSINPVILPFISRDVYRTESLAGINLFLTQPVNGVP
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Bespindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY265167; AAP86782.1; -..
R InterPro; IPR001178; Endotoxin. C.
R InterPro; IPR005639; endotoxin. C.
R InterPro; IPR0085639; endotoxin. C.
R InterPro; IPR008579; Gal_bind_like.
R Pfam; PF03944; Endotoxin. C; 1.
R Pfam; PF03555; Endotoxin. M; 1.
R Pfam; PF03545; Endotoxin. M; 1.
R Pfam; PF03445; Endotoxin. M; 1.
R Pfam; PF03445; Endotoxin. M; 1.
R Pfam; PF03445; Endotoxin. M; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name=cryll,
Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
110-1428;
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Pred. No. 1.9e-252;
2; Mismatches 1;
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databases.
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G) GO:0005022; F:receptor binding; IE
G) GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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95.4%; Score 3589; DB 2;
Best Local Similarity 95.6%; Pred. No. 5.8e-243;
Matches 688; Conservative 14; Mismatches 16;
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Submitted (JUN-2000) to the EMBL/GenBar EMBL; AF218797; AAM73516.1; -- PIR; BA2459; B42459.
HSSP; P02965; LGTY.
GO; GO:0005102; F:receptor binding; IES GO; GO:0006952; P:achogenesis; IEA. InterPro; IPR001178; Endotoxin.
InterPro; IPR00538; endotoxin.
InterPro; IPR005639; endotoxin.
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Pfam; PF00344; Endotoxin.
Pfam; PF00345; Endotoxin.
SEQUENCE 719 AA; 80984 MW; 84F1287;
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                                                                                                    AA; 81230 MW; 42746D478359BBA7 CRC64;
                                                                                                                                           Query Match 98.9%; Score 3718; DB 2; Best Local Similarity 99.2%; Pred. No. 5.1e-252; Matches 714; Conservative 2; Mismatches 2;
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Porcar M., Martinez C., Caballero
       Pfam; PF03944; Endotoxin_C; 1. Pfam; PF00555; Endotoxin_M; 1. Pfam; PF03945; Endotoxin_N; 1. Plasmid.
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                      660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
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                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-UIJ-2004 (Rel. 44, Last annotation update)
05-UIJ-2004 (Rel. 47, Last annotation update)
Pesticidial crystal protein cryllb (Insecticidal delta-endotoxin
Cryll(b)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
Names-ryllb, Synonyms=cryll(b), cryv, cryv465;
Bacillus thuringiensis (subgp. entomocidus).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                  600 KTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEK
                                                                                                                    600 KTFRTVGFTTPFSFSDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entomocidus.";
Appl. Environ. Microbiol. 61:2402-2407(1995).
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.
Active on Plutella xylostella but not on Bombyx mori.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I., Toblestribution of cryv-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryv-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
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InterPro, IPRO01178; Endotoxin.
InterPro, IPRO05638; endotoxin.
InterPro, IPRO05639, endotoxin.
InterPro, IPRO08999; Gal_bind_like.
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MEDLINE-95314293; PubMed-7793960;
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                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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SEQUENCE 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ARNKALTDIKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALBLMFVQKLPSFAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                              STRAIN=BTC007;

MEDLINE=22837682; PubMed=12957903;

Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,

Hu Y., Li G., Huang D.;

"Identification of cryll-type genes from Bacillus thuringiensis
strains and characterization of a novel cryll-type gene.";

Appl. Environ. Microbiol. 69:5207-5211(2003).

EMBL, AF211190; AAG43526.1;

HSSP: P02955; ICIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 719;
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Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.5%; Score 3517; DB 2; 93.1%; Pred. No. 6.5e-238; ive 27; Mismatches 21;
                                                                                                                                               Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005102; F:receptor binding; IEA.
GO; GO:000592; F:receptor binding; IEA.
GO; GO:0009405; F:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005539; endotoxin.C.
InterPro; IPR005539; endotoxin.N.
InterPro; IPR008539; endotoxin.N.
Pfam; PF0344; Endotoxin.C; I.
Pfam; PF0355; Endotoxin.M; I.
Pfam; PF0355; Endotoxin.M; I.
(TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 93.11
Matches 670; Conservative
                                                                                                       Bacillus thuringiensis.
Plasmid pBTC19.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=1428;
                    01-MAR-2001
01-MAR-2004
  01-MAR-2001
                                                                                     Name=cryll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 WGGHKLEFRTIGGTLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
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                  segment of the protein is located
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SEQUENCE 719 AA, 81403 MW, F335F5689D3B0C45 CRC64;
                                                            -!- SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.4%; Score 3363; DB 1;
89.3%; Pred. No. 4.2e-227;
ive 36; Mismatches 39;
                                                                                                                                                                                                                                                                                                                     InterPro; IPR001118; Endotoxin.
InterPro; IPR005638; endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR008979; Gallbind_like.
Pfam; PP03944; Endotoxin_C; 1.
Pfam; PP03945; Endotoxin_M; 1.
                                                                                                                                                                                                                                                                             EMBL; AF047579; AAD44366.1; -
HSSP; P02965; 1CIY.
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Best Local Similarity 89.3%;
Matches 643; Conservative
  the spore coat.
MISCELLANEOUS: Toxic
                                         terminus
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                                                                                                                                                                                                                                                                                                                                                                                             IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM 359
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                                                                                                                             ARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVS
                                                                                                                                                                                                                                             GEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWY
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MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
                                       QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTY
                                                                   OTGIGIAGKILGTLGVPFAGOIASLYSFILGELWPKGKSOWEI-FMEHVEELINOKILTY
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Curr. Microbiol. 41:65-69(2000).
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae. Active on Plutella
xylostella and on Bombyx mori.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part
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BEDIJURE=20374042; PubMed=10919402; Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;

Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;

"Cloning of a new Bacillus thuringiensis cryl1-type crystal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Jocy | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control | Control
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            GEEVPLLPIYAQAANLHLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVRMN 239
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VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
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                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllc (Insecticidal delta-endotoxin Cryll(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein)
Name=cryllc; Synonyms=cryll(c);
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                      STRAIN=C18 / Egypt;
Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
--- EUNCELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
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                                                                                                                                                                                                                                                                                                                                                                 the spore coat. MISCELLANBOUS: Toxic segment of the protein is located
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                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the delta endotoxin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.8%; Score 3341; DB 1;
89.2%; Pred. No. 1.5e-225;
ive 35; Mismatches 41;
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InterPro, IPR001178, Endotoxin.
InterPro, IPR005638, endotoxin.C.
InterPro, IPR005639, endotoxin.N.
InterPro, IPR008979; Gal_bind_Ilke.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00555, Endotoxin_M, 1. Pfam, PF03945, Endotoxin_N, 1. Plasmid, Sporulation, Toxin.
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SEQUENCE
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBb (Insecticidal delta-endotoxin CrylB(b)) (Crystaline entomocidal protein).
                                                                                                                                            360 WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
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                                                                                                     IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM
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STRAIN-MREL B-21110 / EG5847;

Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.,

Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.,

"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins

"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins

"Patchic to lepidopteran insects.",

Patcht number US5322687, 21-UNN-1994.

-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgueptient hilal cells of many lepidopteran larvae.

-I- DEVELOPMENTAL STRGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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-!- SIMILARITY: Belongs to the delta endotoxin family.
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Name=cry1Bb; Synonyms=cry1B(b), cryET5
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HSSP; P02965; ICIY.
InterPro; IPR001178; Endotoxin.
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us-10-019-823b-58.rup

Bacillus

Firmicutes; Bacillales; Bacillaceae;

Bacteria, Firmicu NCBI\_TaxID=1441;

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67 IGVLGVPFAGQLASFYSFLYGELMPSGRDPWEI-FLEHVEQLIRQQVTENTRNTAIARLE 125
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                                                                                                                              Gaps
                                                                                                                              19;
                                                                                                        Length
                                                                                                                              Indels
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfan; PR03944; Endotoxin_C; 1.
Pfam; PR0555; Endotoxin_M; 1.
Pfam; PR0555; Endotoxin_N; 1.
Sporulation; Toxin.
SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 (
                                                                                                       DB 1;
                                                                                                       / Match 64.3%; Score 2417.5; DB 1; Local Similarity 65.3%; Pred. No. 2e-160; les 469; Conservative 90; Mismatches 140;
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Parison N.A.

Bishop A.H., Bone E.J., Ellar D.J.;

Rishop A.H., Bone E.J., Ellar D.J.;

"Cloning of novel Bacillus thuringiensis delta-endotoxin.";

"Cloning of novel Bacillus thuringiensis delta-endotoxin.";

"Lonited (NOV-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithalial cells of insects.

-!- FUNCTION: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o

the spore coat.

-!- SIMILARITY: Belongs to the delta endotoxin family.

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                                                                                                                                                                                                                                                                                                                                          Length 1233;
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R HSSP; P02965; 1CIY.
R InterPro; 1PR001178; Endotoxin. C.
R InterPro; 1PR005639; endotoxin. C.
R InterPro; 1PR008979; endotoxin. N.
R InterPro; 1PR008979; endotoxin. N.
R Pfan; PF03944; Endotoxin. C; 1.
R Pfan; PF03945; Endotoxin. M; 1.
R Pfan; PF03945; Endotoxin. N; 1.
R Sporulation; Toxin A4; 140451 MW; 7318382413529F21 CRC64;
                                                                                                                                                                                                                                                                                                                                          64.3%; Score 2417.5; DB 1;
65.3%; Pred. No. 2e-160;
ive 90; Mismatches 140;
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Matches 469; Conservative
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
50-UUL-2004 (Rel. 4), Last annotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
CrylB(c)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
Name-crylBc; Synonyms=crylBc(c), crylBc;
Bacillus thuringiensis (subsp. morrison)).

PRT; 1233 AA.

STANDARD;

RESULT 13
C1BC BACTM
AC C45774;
DT 30-MAY-2000
DT 05-UUL-2004
DE PESTICIDIAL
DE CTYPE(2) (GN Name=CTYBC);
CSN Name=CTYBC);
CSN Bacillus thu

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PD5517; Q45731.
D05517; Q45731.
D1-NOV-1988 (Rel. 09, Created)
D1-NOV-1988 (Rel. 33, Last sequence update)
D1-SD6 (Rel. 34, Last annotation update)
D5-UTL-2004 (Rel. 44, Last annotation update)
D5-UTL-2014 (Rel. 44, Last annotation update)
D5-UTL-2014 (Rel. 44, Last annotation update)
D5-UTL-2014 (Rel. 44, Last annotation update)
D5-UTL-2014 (Rel. 44, Last annotation update)
D5-UTL-2014 (Rel. 44, Last annotation update)
D6-UTL-2014 (Rel. 44, Last annotation)
D8-UTL-2014 (Rel. 44, Last annotation)
D8-UTL-2014 (Rel. 44, Last annotation)
D8-UTL-2014 (Rel. 44, Last annotation)
D8-UTL-2014 (Rel. 44, Last annotation)
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MEDLINE=88203216; PubMed=3362680;
Brizzard B.L., Whiteley H.R.;
"Nucleotide sequence of an additional crystal protein gene cloned from
Bacillus thuringiensis subsp. thuringiensis.";
Nucleic Acids Res. 16:2723-2723(1988).
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                                                                                                                                                                359 IGGGLNTSTHGATNTSINPVTLRFASRDVYRTBSYAGVLLWGIYLBPIHGVPTVRFNF--
                                                                                                                                                                                                                                                                                    428 VTHP----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS
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                                                                                          IGGTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLF--LTQPVNGVPRVDFHWKF
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-!- DEVELOPMENTAL STAGE: The crystal protein is produced dur sporulation and is accumulated both as an inclusion and
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SEQUENCE FROM N.A.
SPECIES=B.t.entomo
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                                                                                                                                       GTFGDIRVNINPPFAQRYRVRIRYASTIDLQFHTSINGKAINQGNFSATMNRGEDLDYKT 601
                                                                                                                                                                                                                                                                                                                                 FRIVGFTIPFSFLDVQSTFTIGAWNFSSGNEVYIDRIBFVPVEVTYEABYDFEKAQEKVT 661
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Pred. No. 1.1e-148;
8; Mismatches 164; Indels 27;
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GO; GO:0006952; P:defense response; IEA.

GO; GO:0006952; P:defense response; IEA.

GO; GO:0006952; P:defense response; IEA.

GO; GO:0006952; P:defense response; IEA.

GO: GO:0006953; PRO05639; endotoxin.

R InterPro; IPR005639; endotoxin.

R InterPro; IPR009639; endotoxin.

R Pfam; PF03944; Endotoxin.

F Pfam; PF03945; Endotoxin.

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Bacceria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
NCBI_TaxID=1436;
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62.5%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 IGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNF-- 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 RVNVPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRTNTG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 GFGPIRVTVNGPLIQRYRIGFRYASIVDFDFFVSRGGTTVNNFRFLRIMNSGDELKYGNF 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 LGVLGVPFAGQLASFYSFLVGELWPRGRDQWEI-FLEHVEQLINQQITENARNTALARLQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 NAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGAT--GVNM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 ASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 IGGTLNISTOGSINISINPVTLPFISRDVXRIESLAGLNLF--LIOPVNGVPRVDFHWKF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 VTHP-----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595 VRRAFITPPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEABYDLERAQEAVNA 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 AQAANLHILILIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGINNLRGT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 TSTIWYNNNAPSFSAIEAAVVRNPHLLDFLEQVIIYSLLSRWSNIQYMNMWGGHKLEFRI 369
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R PIR; S00873; S00873.

R HSSP; P07130; 1DLC.

R InterPro; 1PR0016138; Endotoxin. C.

R InterPro; 1PR001638; endotoxin. C.

R InterPro; 1PR008979; endotoxin. M.

R Pfam; PF03944; Endotoxin. M.

R Pfam; PF03945; Endotoxin. M.; 1.

R Sporulation; Toxin. M.; 1.

R Sporulation; Toxin. B.

R Sporulation; Toxin. B.

R SEQUENCE 1228 AA; 139647 MW; C8B3A19FB5D98575 CRC64;
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Search completed: October 28, 2004, 18:30:09 Job time : 105.579 secs

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October 28, 2004, 18:10:58; Search time 65.6795 Seconds (without alignments) 3549:224 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMEDIES

Description	Sequence 10, Appl	Sequence 8, Appli	Sequence 10, Appl	Seguence 7, Appli	Sequence 42, Appl	Sequence 10, Appl	Sequence 7, Appli	Sequence 63, Appl	Seguence 23, Appl	Sequence 38, Appl	Sequence 2, Appli	Sequence 25, Appl	Sequence 1, Appli
QΙ	US-10-782-020-10	US-10-782-141-8	US-10-782-096-10	US-10-782-570-7	US-10-428-961-42	US-10-809-953-10	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23	US-10-428-961-38	US-10-614-524-2	US-09-826-660-25	US-10-089-678-1
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9	equence 16,	e 17,	equence 13,	equence 2,		equence 2,	equence 2,	eguence 4,	equence 4,	equence 4,	e 4,	equence 72,	e 28,	quence 2, 1	equence 9,	equence 2,	equence 6,	equence 11,	equence 13,	equence 15,	equence 17,	equence 28,	equence 4,	equence 8,	equence 10	equence 12,	, 0	ednence 8,	e 24	equence 6,	Sequence 7, Appli
US-10-42	7 US	7 US-10-782-09	7 US-10-782-570-	3 US-10-032-717-	4 US-10-414-63	5 US-10-606-320-	7 US-10-746-91	3 US-10-032-717-	US-10-414-6	.5 US-10-606-320-4	US-10-746-91	-10-099-285-	US-10-4	09-756-643	.0 US-09-988-462-9	9	US-10-035-060-	US-09-988-462-	US-09-988-462-1	US-09-988-462-1	US-09-988-462-1	-09-988-46	US-10-136-998A-	US-10-136-99	US-10-136-998A-1	US-10-136-998A	US-10-035-060-	US-10-035-060-	US-10-102-46	US-10-782-141-	US-10-782-096-
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                                                               sequence 10, Application US/10782020; Sublication No. US20040197916A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Carczi, Nadine
APPLICANT: Hardiss, Tracy
APPLICANT: Carci, Michael G.
APPLICANT: Carc, Brian
TITLE OF INVENTION: Methods For Its Use
TITLE OF INVENTION: Methods for Its Use
CURRENT FILING DATE: 2004-02-19
FILE REFERENCE: 045600/274139
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: 05/448,810
PRIOR PILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 11
SOFTHARE: FastSEQ for Windows Version 4.0
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ORGANISM: Bacillus thuringiensis
RESULT 1
US-10-782-020-10
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179 179 239 239 299 299 359 359 419 419 479

Fri Oct 29 15:06:26 2004

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Query Match
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DB 17; Length 719;

99.0%; Score 3724;

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1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                     61 QTGIGTAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEI-FMEHVEEIINQKISTY
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                                                   61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTY
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; ORGANISM: Bacillus thuringiensis
US-10-782-096-10
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APPLICANT: Carozzii, Nacine
APPLICANT: Carozzii, Nichael G.
APPLICANT: Kozziel, Nichael G.
APPLICANT: Carr, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
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TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AXMI-014, A DELTA-ENDOTOXIN GEN
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FYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-782-141-8
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VTALPTSTNPRGLKTDVKDYHIDQVSNLVESLSDSFYLDEKRELFBIVKYAKQLHIBRNM 719
VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                         Sequence 10, Application US/10782096

Publication No. US20040210964A1

GENERAL INFORMATION:
APPLICANT: Carcari, Nadine
APPLICANT: Rargiss, Tracy
APPLICANT: Rozael, Micholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AKMI-009, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274148
CURRENT APPLICATION NUMBER: US/10/782,096
CURRENT APPLICATION NUMBER: 60/446,633
PRIOR APPLICATION NUMBER: 60/446,633
PRIOR PILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Bulm, James A.
APPLICANT: Bulm, James A.
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Chu, Chin-Rei
APPLICANT: Gilmer, May J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Delynuclectides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201-1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
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                                                                                                         Length 719;
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                                                                                                            Score 3724; DB 17;
Pred. No. 1e-305;
2; Mismatches 1;
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7
                                                                                                            99.0%;
al Similarity 99.3%;
715; Conservative
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Best Local S
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publication No. US20040210965A1

GENERAL INPORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargiss, Tracy
APPLICANT: Roziel, Michael G.
APPLICANT: Carr. Brian
TITLE OF INVENTION: AZMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AZMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: AZMI-007, A Delta-Endotoxin Gene and
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TITLE OF INVENTION: AZMI-007, A Delta-Endotoxin Gene and
TITLE AZMI-007, A DELTA-0
                                 Indels
      Pred. No. 1e-305;
2; Mismatches 1;
      Best Local Similarity 99.3%;
Matches 715; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                   LENGTH: 1228
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1 LOCATRION: (200)

1 CHER ILON: The 'Xaa' at location 200 stands for any naturally occurring amin

US-10-428-961-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVDFHWKFVTHPIASDNPYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660 VTALFISINPRGLKIDVKDYHIDQVSNLVESLSDBFYLDEKRELFEIVKYANELHIERNM
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                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                31; Indels
                                                                                                                                                                                                                                                                           Query Match 91.5%; Score 3442.5; DB 14; Best Local Similarity 91.9%; Pred. No. 6.7e-282; Matches 662; Conservative 16; Mismatches 31; I)
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION WMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
LENGTH: 710
                                                                                                                               TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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US-10-809-953-10
. Sequence 10, Application US/10809953
. Publication No. US20040181825A1
. GENERAL INFORMATION:

655 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL: 711

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70 QWEI-FLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKN 99
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                                                                                                                                                                                                                                                                                                                                         INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INVENTION INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.5%; Score 2236.5; DB 10; Length
64.1%; Pred. No. 1.6e-179;
.ive 76; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-00. US20030046726A1-2001
CLASSIFICATION: cDrknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 09/55,504
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/951,715
FILING DATE: 26-COT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenia Biotechnology,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMINICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOOLOGY: linear
MOLECTLE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7
                                                                                                                              Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Bliis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1207 amino acids
                                         Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.1
Matches 441; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                              TITLE OF
RESULT 7
US-09-988-462-7
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publication No. 1920030237111A1

Sequence 63, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Chu, Chih-Rei

APPLICANT: Chu, Chih-Rei

APPLICANT: Mark J.

APPLICANT: Mark J.

APPLICANT: Mark J.

APPLICANT: Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

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APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

PRIOR PRILING DATE: 2003-05-02

PRIOR PRILING DATE: 2000-09-13

PRIOR PLING DATE: 2000-09-15

PRIOR PLING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 63

SEQ ID NO 63

SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ي</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 LVKAFNLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDL 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 QEHTSINGKAINQGNESATMARGEDLDYKTERTVGFTTPFSFLDVQSTFTIGAMNFSSGN 631
                          249 DTRTYPINTSAQLTREVYTDAIGAT--GVMMASMNWYNNNAPSFSAIEAAAIRSPHLLDF
                                                                                                                                                                                                                                                                      339 LEQVIIYSLLSRWSNTQYMNMWGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDV
                                                                                                                                                                                                                                                                                                 307 LEQLTIFSASSRWSNTRHMTYRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDV
                                                                                                                                                                                                                                                                                                                                                                                        159 RSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEIS
                                                                                                                                                                               DIQMYPIKITAQLIREVYIDAIGIVHPHPSFISTIWYNNNAPSFSAIEAAVVRNPHLLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENEL PPEATGOPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRINTIEPNSITOIP
                                                                                         219 TEYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSY
                                                                                                                                                                                                                                                                                                                                                               399 YRTESLAGLNLF--LTQPVNGVPRVDFHWKFVTHP----IASDNFYYPGYAGIGTQLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 EVYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESL
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57.4%; Score 2157.5; DB 14

Best Local Similarity 59.0%; Pred. No. 7.8e-173;

Matches 422; Conservative 103; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           692 SDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 SDEFCLDEKRELLEKVKYAKRLSDERNL 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1227
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; FEATURE:
, OTHER PORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23
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US-10-428-961-38
                                                             Query Match
Best Local S:
Matches 420
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                                                                                  62 IAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEI-PLEHVEHLIRQQVTENTRDTA 120
                                                                                                                                               664
                                                                                                                              184
                                                                                                                                                                                                               241 NIRGINAESWIRYNQFRRDLILGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRIN 300
                                                                                                                                                                                                                                                                                                                                          301 APSGFASTIWFININAPSFSAIEAAVIRPPHLLDFPEQLTIFSVLSRWSNTQYMNYWYGHR 360
                                                                                                                                                                                                                                                                                                                                                                                                         361 LESRTIRGSLSTWTHGNTNTSINPVTLQFTSRDVYRTESFAGINILLTTPVNGVPWARFN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629
                                                             66 IAGKILGTLGVPFAGQVASLYSFILGELMPKGKNQWEILFMEHVEE-INQKISTYARNKA 124
                                                                                                                                                                                            LLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLN 244
                                                                                                                                                                                                                                                          245 NIRGINAESWVRYNQFRRDMILMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAIGTVH 304
                                                                                                                                                                                                                                                                                                                         305 PHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWWGGHK 364
                                                                                                                                                                                                                                                                                                                                                                                        LEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFH 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASHV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTF 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAPVYSWIHRSADRINISSDSIIQIPLVKSFNLNSGISVVSGPGFTGGDIIRTNVNGSV 540
                    APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Nara, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: DATE
SSNAKVDKISTDSLKN-----ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIG
                                                                                                                           LIDLKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSGEEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABFPVGISASGSQ-TAGISISNNAGROTFHFDKIEFIPITATFEAEYDLERAQEAVNALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih.Rei
APPLICANT: Chu, Chih.Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201--1
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
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                                                                                                             13 SSNAKVDKISTDSLKN-----ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIG
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tch 57.0%; Score 2142.5; DB 9; Length 1186; al Similarity 58.7%; Pred. No. 1.4e-171; 420; Conservative 106; Mismatches 174; Indels 15;
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Publication No. US20030237111A1
GENERAL INFORMATION:
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APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Van Rie, Jeroen
TITLE CNIVENION: Insecticidal proteins from Bacillus thuringiensis.
FILE REFERENCE: NEWETSUS.
CURRENT APPLICATION NUMBER: US/10/614,524
CURRENT APPLICATION NUMBER: US/09/739,243
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13.
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1228
                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2
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PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 1228
                                                                                                 ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38
                                                                                                                                                                  al Similarity 59.2%
423; Conservative
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Matches 423
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                                                                                                                            1 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI
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                                                                                               13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVEPFVSASTIQTGIAGKI
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                                                  Gaps
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Length 1228;
                                                  Indels
Query Match 55.5%; Score 2087; DB 15;
Best Local Similarity 59.2%; Pred. No. 7.2e-167;
Matches 423; Conservative 96; Mismatches 183;
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RESULT 12 US-09-826-660-25

Sequence 2, Application US/10614524; Publication No. US20040016020A1; GENERAL INFORMATION: APPLICANT: Annaut, Greta APPLICANT: Boets, Annemie APPLICANT: Damme, Nicole APPLICANT: Mathieu, Eva

RESULT 11 US-10-614-524-2

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Sequence 1, Application US/10089678
Publication No. US20030017967A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, ITILE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
TITLE OF INVENTION: 1202-05-02
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/10/089,678
PRIOR APPLICATION NUMBER: PT/JP01/06660
PRIOR APPLICATION NUMBER: PT/JP01/06600
PRIOR PILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
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45.1%; Score 1694.5; DB 14; Lengt
Best Local Similarity 47.7%; Pred. No. 1.1e-133;
Matches 360; Conservative 125; Mismatches 219; Indels
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                                RESULT 13
JS-10-089-678-1
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                                                             APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-14XC2DI
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 2010-04-023
PRIOR APPLICATION NUMBER: 09/178,22
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR PLING DATE: 1999-10-23
PRIOR PLING DATE: 1999-10-23
PRIOR FILING DATE: 1999-13-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PARCELLIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1909.5; DB 9; Length 643; ; Pred. No. 2.7e-152; 99; Mismatches 159; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25
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Sequence 25, Application US/09826660 Patent No. US20010026940A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                     APPLICANT: Cardineau, Guy A.
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Best Local Similarity 57.6%
Matches 371; Conservative
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                                                                                    537 R-RTNTGTF---GDIRVNIN-PPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATM 591
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49.1%; Pred. No. 2.1e-129;
iive 96; Mismatches 229; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: AAMI-014, A Delta-Endotoxin Gene and TITLE OF INVENTION: Methods for Its Use
TITLE REPERENCE: 045600/27443
CURRENT APPLICATION UNBER: US/10/782,141
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/449,632
PRIOR PILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PRASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-782-141-16
US-10-782-16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
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APPLICANT: Hargiss, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Carr, Nicholas B.
APPLICANT: Carr, Brian
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APPLICANT: Baum, Vannes A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Chu, Chih-Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Delynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECOZO1-1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 6
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                       647 DSFASGGEVYVDKFELIPVNATFEAEBDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNQA 705
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44.1%; Score 1658.5; DB 14; Length
Best Local Similarity 51.4%; Pred. No. 4.7e-131;
Matches 346; Conservative 105; Mismatches 173; Indels
                                                                                                                                           Sequence 6, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
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; ORGANISM: Bacillus thuringiensis
US-10-428-961-6
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US-10-428-961-6
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                                                                                                                                                          640 LSMGDFSSGGEVYIDRIEFIPVDETYEARQDLEAAKKAVNALFTNTKD-GLRPGVIDYEV 698
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Perfect score:
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1: geneseqp1980s:\*
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4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Searched:

Run on:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aab66911 Insectici Aab66908 Insectici Aab66908 Insectici Aab66909 Insectici Aaa36273 B. thurin Aaa36273 B. thurin Aaa36274 B. thurin Aaa36274 B. thurin Aaa36274 B. thurin Aaa36274 B. thurin Aaa36274 B. thurin Aaa36271 B. thurin Aaa36271 B. thurin Aaa36271 B. thurin Aab66912 Insectici Aaa36271 B. thurin Aab66912 Insectici Aaa36271 B. thurin Aab66912 Insectici Aaa40609 Bacillus Abb07073 Bacillus Aab6918 B. thuring Adk98489 B. thuring Adk98481 B. thuring Adk98481 B. thuring Adk98481 B. thuring Adk98481 B. thuring Adk98481 B. thuring
SUMMARIES	AAB66911 AAB66909 AAB66909 AAB66909 AAB56273 AAB66910 AAB56274 AAU2095 AAN08041 AAB66907 AAB66907 AAB66907 AAB66907 AAB66907 AAB66907 AAB66907 AAB669089 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093 AAU2093
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Gaps

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Query Match 99.3%; Score 3736; DB 4; Length 719; Best Local Similarity 99.7%; Pred. No. 1.1e-291; Matches 718; Conservative 0; Mismatches 0; Indels 2

Aar54074 CrvET5, 2	Aaw35259 Bacillus	Aaw17699 CryET5. 3	Aaw87633 CryETS pr	Aay30923 B. thurin	Adk98479 B thuring	Aaw44322 Bacillus	Aab19947 Bacillus	Aar50955 Bacillus	Aau02094 Bacillus	Aay31990 Chimeric	Aaw44321 Bacillus	Aab19950 Bacillus	Aau02046 B. thurin	Aay16796 Amino aci	Aau00421 B. thurin	Aau00420 B. thurin	Aab84628 Amino aci	Aau02039 B. thurin	Aay16797 Amino aci
AAR54074	AAW35259	AAW17699	AAW87633	AAY30923	ADK98479	AAW44322	AAB19947	AAR50955	AAU02094	AAY31990	AAW44321	AAB19950	AAU02046	AAY16796	AAU00421	AAU00420	AAB84628	AAU02039	AAY16797
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64.3	64.3	64.3	64.3	64.3	64.3	61.6	61.6	59.8	59.7	59.4	57.6	57.6	57.4	57.0	56.6	56.2	55,5	55.5	50.8
2417.5	2417.5	2417.5	2417.5	2417.5	2417.5	2318.5	2318.5	2250.5	2244.5	2235.5	2166.5	2166.5	2157.5	2142.5	2127.5	2113.5	2087	2087	1909.5
	27		53	30	31	32	33	34	32	36	37	38	39	40	41	42		44	4.5

# ALIGNMENTS

ESU	RESULT 1
903	ası. AAB66911 standard, protein, 719 AA.
S S S S	AAB66911;
(E)	12-APR-2001 (first entry)
· 图:	Insecticidal protein crylla5.
{∑}	Insecticide; transgenic plant; insect-resistance.
\$ 8 \$	Paecilomyces sp.
¥ & }	W0200100841-A1.
₹£!	04-JAN-2001.
X E	23-JUN-2000; 2000WO-GB002457.
<b>4 K K</b> I	29-JUN-1999; 99GB-00015215. 23-DEC-1999; 99GB-00030536.
X & S	(ZENE ) ZENECA LTD.
X II II X	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ; Vincent JL, Lee MD;
(音)	WPI; 2001-123015/13.
SEE EE X	Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
S X	Claim 14; Page 62-64; 72pp; English.
\$888888	The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66895 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
S S	Sequence 719 AA;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringtensis insecticidal crivity. The present sequence is sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
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                                                          comprising an X-glycine motif a
                                                                                                                                                                                                                                                                                                                                     Score 3736; DB 6;
Pred. No. 1.1e-291;
); Mismatches 0;
                                                                                                            Claim 12; Page 53-56; 67pp; English
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                                                              New insecticidal protein compr
terminus, useful as an active
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Best Local Similarity 99.7%;
Matches 718; Conservative (
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                               WPI; 2003-175137/17
Viner
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Vincent JL,
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   MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                 OTGIGIAGKILGTLGVPFAGOVASLYSFILGELWPKGKNOWBIMPWEHVEE, INOKISTY
                      MKLKNQDKHQSFSSNAKVDKISTDSLKNBTDIELQNINHEDCLKMSEYENVEPFVSASTI
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Indels Length

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VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 

KTERTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIBFVPVEVTYBAEYDFEKAQEK KIFRIVGFITPPSFLDVQSTFIIGAMNFSSGNEVYIDRIEFVPVEVIYBAEYDFEKAQEK

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07-JUN-2001; 2001GB-00013900. 30-MAY-2002; 2002WO-GB002666

RESULT 2 AAE36275

(SYGN ) SYNGENTA LTD

539 539 50 90 599 629 629 719

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The present invention relates to novel insecticidal proteins obtained from Paccilomyces sp. (see AAB6689) to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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Pred. No. 1e-290;
1; Mismatches 1;
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99GB-00030536.
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llarity 99.4%;
Conservative
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23-DEC-1999;
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Best Local Simi
Matches 716;
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                                            protein, crylla3
                                                              endotoxin;
                                                             pesticide; insecticidal crystal
                                           B. thuringiensis insecticidal crystal endotoxin (CRY)
                                                                                                                                                                 07-JUN-2001; 2001GB-00013900
                                                                                                                                            30-MAY-2002; 2002WO-GB002666
                                                                                  Bacillus thuringiensis
                                                                                                                                                                                    (SYGN ) SYNGENTA LTD
                                                                                                     WO200298911-A2
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motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal activity, The present sequence is sequence is used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
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insecticidal protein comprising an X-glycine motif ands, useful as an active ingredient of a pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 3724; DB 6;
Pred. No. 1e-290;
1; Mismatches 1;
                                                                                                  Claim 12; Page 47-50; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.4%;
Matches 716; Conservative
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                                            terminus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel insecticidal proteins obtained from Paccilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                           660 VIALFISTNPRGIKTDVKDYHIDQVSNLVESISDBFYLDEKRELFEIVKYAKQLHIERNM
                                                                                                                                                                                                                                                                                     660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                                                                         480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
                                                                                                                                               480 SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
                                                                                                                                                                                                                                540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY
                                                                                                                                                                                                                                                                  600 KTFRTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEK
             360 WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
                                                    RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
                                                                                                                                                                                              540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY
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Pred. No. 2.2e-290;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66910 standard, protein; 719
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99GB-00030536.
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Best Local Similarity 99.2%;
Matches 714; Conservative
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Lee MD;
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Vincent JL,
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                                                                                                                          protein, crylla2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the amino-
                                                                                                                                                          Insecticidal protein; pesticide; insecticidal crystal endotoxin;
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Pred. No. 1e-290;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insecticidal protein comprising an X-glycine motif a terminus, useful as an active ingredient of a pesticide.
                                                                                                                          B. thuringiensis insecticidal crystal endotoxin (CRY)
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                    Ā
                  AAE36272 standard; protein; 719
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hes 715, Conservative
                                                                                                                                                                                            Bacillus thuringiensis
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AAE36272
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al Similarity 99.2%;
714; Conservative
         Viner R;
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         Vincent JL,
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Best Local S:
Matches 714,
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                                                         QTGIGIAGKILGTLGVPPAGQVASLYSFILGELWPKGKNQWEI-FMEHVEEIINQKISTY
                                                                                               ARNKALTDLKGLGDALAVYHDSLESMVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVS
                                                                                                                                                                                                             RVDFHWKFVTHPIASDNFYYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
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                          MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                              QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTY
                                                                                    ARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVS
                                                                                                                        GEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY
                                                                                                                                          GEEVPLLPIYAOAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY
                                                                                                                                                              STGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDA
                                                                                                                                                                                                                                        WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
                                                                                                                                                                                                                                                        WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
                                                                                                                                                                                                                                                                              RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
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                                                                                                                                                                                                                                                                                                                                                                    NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDY
                                                                                                                                                                                                                                                                                                                                                                                           KTFRIVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFEKAQEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. thuringiensis insecticidal crystal endotoxin (CRY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; pesticide; insecticidal crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE36274 standard;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringienes; sinsecticidal crivity. The present sequence is sequence is used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QTGIGIAGKILGTLGTLGTLGTLGTLGTVSFILGELWPKGKNQWEI-FMEHVEEIINQKISTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEEVPLIPIYAQAANLHILLIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY
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    amino
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New insecticidal protein comprising an X-glycine motif at the terminus, useful as an active ingredient of a pesticide.
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Pred. No. 2.2e-290;
2; Mismatches 2;
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(SYGN ) SYNGENTA LTD

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180 GEEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWY 239
                                                                                                   300 IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                             VTALFTSTNPRGLKTDVKDYHIDQVSNLVBSLSDBFYLDBKRELFEIVKYAKQLHIERNM
                                           STGINNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDA
                                                                                                                                                            360 WGGHKLEFRTIGGTLNISTQGSTNTSINEVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera
                              STGLINNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDA
                                                                                  IGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM
                                                                                                                                           WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP
                                                                                                                                                                                                  RVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI
                                                                                                                                                                                                                  SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
                                                                                                                                                                                                                                                                                                                 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY
                                                                                                                                                                                                                                                                                                                                                                                                  600 KTFRTVGFTTPFSFLDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence carried on pJH12 which was isolated from B. thurinstrains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kD endotoxin deduced from DNA carried on pJH12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crystal; insecticide; toxin; delta endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis; JHCC 4353 and 4835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR08041 standard; protein; 719 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Fig 5-10; 66pp; English
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N-PSDB; AAQ06636.
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25-MAR-2003
27-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEILFMEHVEE-INQKISTY 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVS 179
                                                                                                                                                              protein; Crylla; CrylBa; moth; butterfly; Colorado potato beetle;
mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is B. thuringiensis (Bt) crystal protein Crylla, the DNA encoding which was mutated to allow cloning of domain III or domains I and II, to make the hybrid protoxins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEI-FWEHVEEIINQKISTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3715; DB 4;
Pred. No. 5.4e-290;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
                                                                                                                                                Bacillus thuringiensis partial mutant Crylla.
                                                                                                                                                                                                                                                              1. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                         20. .719 ___/label= Mature_Crylla
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 30-32; 43pp; English.
                                                               AAU02095 standard; protein; 719 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-00203723
                                                                                                                     (first entry)
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                                                                                                                                                                                                                     Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosch HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-337141/36.
N-PSDB; AAS04855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 719 AA;
                                                                                                                                                                                                                                                                                                                                     EP1099760-A1
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                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-1999;
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                                                                                                                     07-SEP-2001
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                                                                                        AAU02095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insects.
                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                             Crystal
                                                                                                                                                                                                                                                                                          Protein
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Dp ò g

g  $\delta$ 

amino

at the

2002WO-GB002666

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New insecticidal protein comprising an X-glycine motif a terminus, useful as an active ingredient of a pesticide
                                                                                                                                                                                                                                Claim 12; Page 42-44; 67pp; English
                                                                                                     07-JUN-2001; 2001GB-00013900.
            Bacillus thuringiensis.
                                                                                                                                                 JL, Viner R;
                                                                                                                            (SYGN ) SYNGENTA LTD
                                                                                                                                                                        WPI; 2003-175137/17
                                    WO200298911-A2
                                                                               30-MAY-2002;
                                                         12-DEC-2002
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be used to produce transformants B.coli strain MC12022/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                                                MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                      MKLKNODKHOSFSSNAKVDKISTDSLKNETDIELONINHEDCLKMSEYENVEPFVSASTI
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                                                                                                                            Gaps
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                                                                                                      Length 719;
                                                                                                                           Indels
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                                                                                                  Score 3703; DB 2;
Pred. No. 5e-289;
2; Mismatches 4
                                                                                                 98.5%;
                                                                                                             Local Similarity 98.9
                                                                             Sequence 719 AA;
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or symergicic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is sequence is used in the invention
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Pred. No. 3.5e-288;
?; Mismatches 3;
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Best Local Similarity
Matches 712; Conserv
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cryllal

Insecticidal protein; pesticide; insecticidal crystal endotoxin;

B. thuringiensis insecticidal crystal endotoxin (CRY) protein,

(first entry)

26-JUN-2003

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protein; 718

standard;

AAE36271

AAE36271

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Bacillus thuringiensis cryl gene, expression vector, nucleotide sequence with high-toxicity to lepidoptera pests, encoded protein, primer sequences and the shuttle vector pSXX422b, useful as a pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                     GEEVPILDIYAQAANLHILLIRDASIFGKEWGLSSSBISTFYNRQVERAGDYSYHCVKMY
                                                                                                                               300 IGTVHPHPEFISTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNM
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N-PSDB; ADM74716.
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                                                                                                                                 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSSLSDEFYLDEKRELFEIVKYAKQLHIERNM 718
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                                                                             VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                                                            KTFRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEK
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                          NIGTFGDIRVNINPPFAQRYRVRIRYASTIDLQFHISINGKAINQGNFSAIMNRGEDLDY
   NIGIFGDIRVNINPPFAQRYRVRIRYASTIDLQFHISINGKAINQGNFSAIMNRGEDLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.0%; Score 3686.5; DB 4; Length 718; 98.8%; Pred. No. 1.1e-287; ive 2; Mismatches 4; Indels 3;
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                                                                                                                                                                                                                                                                                                                                           Insecticide; transgenic plant; insect-resistance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mackay EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cayley PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 53-55; 72pp; English.
                                                                                                                                                                                                                        AAB66907 standard; protein; 718
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Matches 711; Conservative
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                                                                                                                                                                                                                                                                                                               Insecticidal
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23-DEC-1999;
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Insecticide, transgenic plant, insect-resistance.
                                                                                                                                                                                                                                                                                                               Claim 14; Page 64-66; 72pp; English
            Insecticidal protein cryllb1
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                                                                                                                                                                                                        Carlile AJ,
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controlling insects,
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         The invention relates to a novel Bacillus thuringiensis cryl gene, gene combination, expression vector, nucleotide sequence of the B thuringiensis cryl gene with high-toxicity to lepidoptera peets and the amino acid sequence of the protein encoded by it, cooperative use of the cryl gene with the expression product of crylab or crylBa, primer sequences for expressing the genes, and the constructed shuttle vector pSX422b. The gene in combination with the crylab or crylab genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the cryllel protein.
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                                                                                                                                                Query Match 93.5%; Score 3517; DB 7; Length 719; Best Local Similarity 93.1%; Pred. No. 4.8e-274; Matches 670; Conservative 27; Mismatches 21; Indels
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Warner

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Mackay

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Cayley

99GB-00015215.

protein obtained from species of Paecilomyces s, and for insect-resistant transgenic plant

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The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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                                                                                                                                                                                    92.6%; Score 3484; DB 4;
92.2%; Pred. No. 2.2e-271;
ive 33; Mismatches 21;
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719

standard; protein;

AAB66912

AAB66912,

(first entry)

12-APR-2001

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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crivity. The present sequence is sequence is used in the invention
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                                          SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT
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SASHVKALVYSWIHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFIGGDILRRI
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RESULT 2 insecticidal protein cryV - Bacillus thuringiensis c;species: Bacillus thuringiensis C;species: Bacillus thuringiensis C;species: Bacillus thuringiensis C;species: Bacillus thuringiensis C;scession: I39815 R;dlaeve, A. P.; Williams, R.; Heagence_revision 19-Jul-1996 #text_change 09-Jul-2004 C;Accession: I39815 A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for lensis subset) A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for lensis subset) A;Reference number: I39815; MUD:93298009; PMID:8517758 A;Accession: I39815 A;Accession: I39815 A;Accession: I39815 A;Accession: I39815 A;Readuse: I-719 <res> A;Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768 C;Genetics: A;Gene: cryv C;Superfamily: parasporal crystal protein</res>	1 - Bacillus thuringiensis n; parasporal crystal protein ision 17-Apr-1993 #text_change G.; Pells, S.; Pike, D.; Jorda crerization of a novel Bacillu 92269582; PMID:1588820 2; EMBL:X62821; NID:g40289; PI protein
Query Match Best Local Similarity 92.9%; Pred. No. 2e-242; Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;	Query Match 93.8%; Score 3511; DB 2; Length 719; Best Local Similarity 92.8%; Pred. No. 8.7e-242; Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;
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Qy 121 RNKALSDLRGLGDALAVYHESLESWYENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG 180	OY 121 RNKALSDIRGLGDALAVYHESIBSWVENRNNTRARSVVKNOYIALEIMFVQKLPSFAVSG 180
QY 181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN 240	OY 181 EEVPLLETYAQAANLHLILIRDASIFCKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN 240
QY 241 TGLMNLRGTNAKSWVRYNQFRKDMTLMVLDIVALFBSYDTLVYPIKTTSQLTREVYTDAI 300 	OY 241 TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI 300 
QY 301 GTVHDNQAFASTTWYNNNAPSFSAIZAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMW 360	OY 301 GTVHPNOAFASTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTOYMMW 360       :
OY 361 GGHKLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGINLFLTQPVNGVPR 420	Qy 361 GGHKLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVXRTESLAGLNLFLTQPVNGVPR 420

QY	540 QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540 Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540 540	Oy   541 TGTFGDIRVNINPPRAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 609	660 QY 601 TFRIIGFTTPPSFSDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEXDEKAQEKV 660     -	QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719  DD 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719	PRESEUT 5  SOURCE 1  PRICATE THE CANADA PROCESS OF CANADA - Bacillus thuringiensis subsp. thuringiensis  NALICHERATE AND #ASSERGED CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA PROCESS OF CANADA
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- Bacillus thuringiensis ryIH 000 #text_change 09-Jul-20 S.; Piens, C.; Saey, B.; crystal protein with a hig :8572715 ; NID:9547554; PIDN:CAA857 ive against corn borer and bB 1; Length 1157; 217; Indels 80; Gaps	29 LASDENAALQNWANKEDILAGESTEET STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES	OY 258 NOFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGTVHPNQAFASTTWYNN 317  269 HQFREMTLVVLDVVALFPYTSNPGNPQLTREVYTDPIVPNPPANVGLCRRWGTN 328  QY 318 NAPSFSALEAAVIRSPHLLDFLEKVITSLLSRWS-NTQYMNWWGGHRLESRPIG-GALN 375  Db 329 PYNFSELENAFIRPPHLEDRINSLTISSNRFPVSSNFMDYWSGHTLRRSYLNDSAVQ 386  QY 376 TSTQGSINTSINPVTLQFTSRDVYRTESLAGLNLF-LTQPNV 416	Db 387 EDSYGLITTRATINPGVDGTNRIESTAVDFRSALIGIYGVNRASFVPGGLFNGTTSPAN 446  Qy 417 GVPRVDFHWKFPTLPIASDNFYYLGYAGVGTQLODSENELPP-ETTGQPNYESYSHRISH 475  Db 447 GGCR	OY 527 GPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRURIRYASTTDLQFHTSINGKAINQGN 586	OY 641 VPVEVTYEAEXDEEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEK 700
ETTGQPNYESYSHRLSHIGLISASHVKAL 487  ETTERPNYESYSHRLSHIGH	hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag Cippedes: Bacillus thuringiensis Cippedes: Bacillus thuringiensis Cipacies: Bacillus thuringiensis Cipace: 10-Uul-1922 #sequence_revision 10-Uul-1992 #text_change 09-Uul-2004 Cipacession: B42459 Richambers: U.A.; 'Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C. J. Bacterric. U.A.; 'Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C. A.Reference number: A42459; MUD:91286178; PMID:2061280 A; Accession: B42459 A; Status: preliminary A, Robecule type: DAA A; Robecule type: DAA A; Robecule type: DAA A; Robecule type: DAA A; Cross-references: UNIPROT:Q8KY61; UNIPROT:Q45740; GB:M63897 C; Superfamily: parasporal crystal protein	Query Match         48.5%; Score 1813; DB 2; Length 380;           Best Local Similarity 90.3%; Pred. No. 2.5e-121;           Matches 343; Conservative 24; Mismatches 13; Indels 0; Gaps 0;           Qy           MKLKNPDKHQSLSSNAKVDKTATDSLKNETDIELKNANNEDYLRNSEHESIDPFVSASTI 60           Db           MKLKNPDKHQSSSNAKVDKISTDSLKNETDIELKNANNEDYLRNSEHESIDPFVSASTI 60           Db           MKLKNPDKHQSSSNAKVDKISTDSLKNETDIELKNANNEDFVSEYSTI 60           QY         61 QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQMEIFMRHVEETINQKILTYA 120	Db 61 QTGISIAGKILGTLGVPFAQVASIYSFILGELWPKGKNOWEIFWEHVEEIINQKLSTYA 120  Qy 121 RNKALSDLRGLGDALAVYHESLESWVENRNYRARSVVKRQYIALELMFVQKLPSFAVSG 180	OY 241 TGLNNLRGTNAKSWVRYNOPRKOMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI 300  241 TGLNNLRGTNAESWVRYNOPRKOMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI 300  QY 301 GTVHPNQAFASTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWW 360  DD GTVHPNASFASTTWYNNNAPSFSTIESAVVRNPHLLDFLEKVTIYSLLSRWSNTQYMNWW 360	Qy 361 GGHRLESRPIGGALNTSTQG 380  Db 361 GGHRLEFRTIGGMLNTSTQG 380

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parasporal crystal protein crylFa3 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: $32649
R:Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Reference number: $32645
A;Accession: $32649
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Crase-references: UNIPROT:045749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g29586
C;Superfamily: parasporal crystal protein
C;Sywords: delta-endotoxin
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39.9%; Score 1491.5; DB 2; Length
Best Local Similarity 47.4%; Pred. No. 1.2e-97;
Matches 323; Conservative 88; Mismatches 179; Indels
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c;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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46.6%; Pred. No. 1.6e-98;
ive 97; Mismatches 210; Indels
KMLLEAVRAAKRLSRERNL 732
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Matches 330; Conserv
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256 RYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGTVHPNQAFASTTWY 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: cry-1-2; bt2
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
Fy2-586/Product: toxic peptide #status predicted
F;82-300/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
                                                                                                                                                                             A)Molecule type: mRNA
A)Residues: 1-1155 <KON>
A)Cross-references: UNIPROT:P06578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A91560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: A26461
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C;Species: Bacillus thuringlensis
C;Species: Bacillus thuringlensis
C;Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004
C;Accession: A26513
R;Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
Gene 53, 113-119; 1987
A;Title: Nuclectide sequence of the insecticidal protein gene of Bacillus thuringiensis
A;Reference number: A26513
A;Accession: A26513
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A;Accession: A2
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N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal
C;Species: Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                     Score 1487.5; DB 2; Length
Pred. No. 2.2e-97;
5; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 46.4%; Promatches 309; Conservative 106;
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A; Molecule type: DNA
A; Residues: 1.1155 < GEI>
A; Residues: 1.1155 < GEI>
A; Residues: 1.1155 < GEI>
A; Cross-references: GE: Mills 271; NID: g143123; PIDN: AAA22561.1; PID: g143124
A; Experimental source: subsp. kurstaki
B; Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
BNA 5, 305-314, 1986
A; Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product analy
A; Reference number: A90955; WUID: 86300092; PMID: 3743328
A; Accession: A90955
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1155 CGHA>
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
B;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckh
Bir. J. Biochem. 161, 273-280, 1986
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri
A;Reference number: A26461; MUID:87054026; PMID:3023091
                                                                                                                                                                                                                                                                                                                                                                                                 A.Experimental source: subsp. kurstaki
R.Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A.Title: The hypervalable region in the genes coding for entomopathogenic crystal protes
A.Reference number: A91560; MUID:87163505; PMID:3557124
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes A;Reference number: A90025
A;Accession: A90025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Residues: 11155 cWAB>
A)Residues: 11155 cWAB>
A)Ross-references: GB:N13898, NID:G142719, PIDN:AAA22330.1; FID:G142720
A)Experimental source: subsp. berliner
R)Chak, R.P.; Jen, J.C.
R)Chak, R.P.; Jen, J.C.
R)Chak, R.P.; Dena Library, October 1990
A)Bescription: Complete nucleotide sequence and expression in Escherichia coli of A)Reference number: S14555
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A;Residues: 1-730, 'L',732-784,'R',786-1155 <HOF>
A;Cross-references: GB:XO4698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A;Experimental source: strain berliner 1715
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 HILLIRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYNTGLNNLRGTNAKSWV
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Aptretriate hadres data-endocoxin 10.1; enconocidal crystal process of pacific strain alzawai IC1
Cypecies: Bacillus thuringiensis
A;Variety: strain alzawai IC1
Cypecies: Bacillus thuringiensis
A;Variety: strain alzawai IC1
Cypecession: 802134; 804994
R;Haider, M.Z.; Ellar, D.J.
R;Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A;Title: Nucleotide sequence of a Bacillus thuringiensis alzawai IC1 entomocidal crystal A;Reference number: 802134; MUID:89083518; PMID:3205732
A;Reference number: 802134
A;Reference number: 802134; MUID:89083518; PMID:3205732
A;Residues translation not shown
A;Residues: 1-1155 cHAI>
A;Rocosine: Source: strain alzawai IC1
R;Haider: M.Z.; Ellar, D.J.
A;Cross-references: UNIPROT:P06578; EMBL:X13233; NID:940277; PIDN:CAA31620.1; PID:940278
A;Eferences: UNIPROT:P06578; PMID:2769751
A;Cross-references: Source: strain alzawai IC1
A;References: 204994; MUID:89362455; PMID:2769751
A;Rocoule type: DNA
A;References: EMBL:X16315
A;Rocoule type: DNA
A;Residues: 429-449; Ax, 451-724 cHAW>
A;Rocoule type: DNA
A;Residues: 429-449; Ax, 451-724 cHAW>
A;Rocoule type: DNA
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N/Alternate names: delta-endotoxin IC1; entomocidal crystal protein
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                                                           274 ENFDGSFRGSAQGIEGS-IRSPHLMDILNSITIYTDAHR---GEY--YWSGHQIMASPVG 327
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                          316 NNNAPSF----SAIBAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMWGGHRLESRPIG 371
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                                                                                                                                                            328 FSGPEFTFPLYGTWGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 FEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 RVDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLI
                                                                                                                                                                                                                                                                                                                                                                 GDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGEDLDYKTFRTIGFTTPFSFSDVQSTFTIGAMNFSSGNEVYIDRIEFVPVEVTYBAEYD
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                                                                                                                                                                                                                                                                                  385 GTEFAYG-----TSSNLPSAVYRKSGT--VDSLDEIPPQNNNVPPRQGFSHRLSHVSMF
                                                                                                                                                                                                                                                                                                                                   ----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTG
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39.1%; Score 1463.5; DB 2;
Best Local Similarity 46.0%; Pred. No. 1.1e-95;
Matches 307; Conservative 105; Mismatches 198;
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Barasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki
C;Species Dec-1888 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29125
R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme Bio/Technologis, 5, 807-813, 1987
A;Technologis A;Pernat transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Status: not compared with conceptual translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                             RSGFSNSSVSIIRAPMFSWIHRSABFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTG 496
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                                                                        NNNAPSF----SAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWGGHRLESRPIG 371
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A, Residues: 1-1156 <FIS>
C, Cross-references: UNIRROT: 09F296; UNIPROT: 093T21
C, Superfamily: parasporal crystal protein
C, Keywords: delta-endotoxin
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Best Local Similarity
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parasporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: 13938
E;Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
J. Blotechnol. 6, 307-322, 1987
A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstakin
A;Accession: 13938
A;Accession: 13938
A;Accession: 13938
A;Accession: 13938
A;Accession: 13938
A;Accession: 13938
A;Accession: 1395 ABSS
A;Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                           SGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTFYRNPFIIGIN---NQRLSVLDG
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                             HILLIRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYNTGLNNLRGTNAKSWV
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                                                                                                                                                       NNNAPSFSAIEAAV---IRSPHLLDFLEKVTIYSLLSRWSNTQYMNMWGGHRLESRPIG-
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                                                                                                             Query Match 39.1%; Score 1461.5; DB 2; Best Local Similarity 46.2%; Pred. No. 1.6e-95; Matches 308; Conservative 103; Mismatches 199;
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A41052
parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
c)species: Bacillus thuringiensis
C).Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C).Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C).Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C).Date: 03-Aproson: A41052
R).Bacteriol. 173. 6655-6638, 1991
A.Reference number: A41052; MUID:92011442; PMID:1655719
A.Accession: A41052
A.Accession: A41052
A.Accession: DAA
A.Residues: 1-1181 class
A.Accession: A41052
A.Accession: A41052
A.Accession: A41052
A.Accession: A41052
A.Accession: A41052
C).Residues: 1-1181 class
C).Residues: 1-1181 class
C).Residues: 1-1181 class
C).Residues: 1-1181 class
C).Respacefamily: parasporal crystal protein
C).Reywords: delta-endotoxin
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    AVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANL
                        RYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGTVHPNQAFASTTWY
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                                                                HLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYNTGLNNLRGTNAKSWV
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                                                                                                                                             Score 1463.5; DB 2; Length
Pred. No. 1.2e-95;
1; Mismatches 201; Indels
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Best Local Similarity 45.9%; Pri
Matches 306; Conservative 104;
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LSDERNL 683
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Search completed: October 28, 2004, 18:32:04 Job time : 26.191 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model October 28, 2004, 17:52:12 9

/ Search time 98.4365 Seconds
(without alignments)
4202.652 Million cell updates/sec

US-10-019-823B-59 3742 1 MKLKNPDKHQSLSSNAKVDK......KRELFEIVKYAKQIHIERNM 719 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### CITAMANDIDO

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SUMMARIES	QI	CIIB BACTE	Q9F0P8	Clic_BACTU	C11A_BACTK	Q6X1 <u>8</u> 1	AAP86782	Q93NJ5	085796	CAC85964	Q8KY61	C1ID BACTU	C1BB_BACTU	C1BC_BACTM	Q93T75	C1BA_BACTK	Q93NM5	Q6PYW8	AAS93797	C1BE_BACTU	QBKN <u>Y</u> 2	CIBD_BACTZ	C1KA_BACTM	Q45740	Q8KZL7	CBAA BACUK	C9CA_BACTO	C1GA BACTU	C1FB_BACTM	Q45749	C8BA_BACUK	C1AB_BACTK
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# **ALIGNMENTS**

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                               30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllb (Insecticidial delta-endotoxin
Cryll(b)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
Namescryllb; Synonyms=cryll(b), cryV, cryV465;
Bacillus thuringiensis (Bacillates, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                      the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                           STRAIN=BP465; MEDLINE=95314293; PubMed=7793960; MEDLINE=95314293; PubMed=7793960; Roo B.T., Lee S.T., Kim J.I.; Shin B.-2., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.; Instribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81295 MW; E8210ABEAE97688E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the delta endotoxin family.
              719 AA
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InterPro; IPR005638; endotoxin_C.
InterPro; IPR008659; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PF03944; Endotoxin_C; I.
Pfam; PF03945; Endotoxin_M; I.
Pfam; PF03945; Endotoxin_M; I.
                PRT;
                                                 30-MAY-2000 (Rel. 39, Created)
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                STANDARD;
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SEQUENCE 719 AA;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Gaps

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TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWRGEDLDYK 600
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strains and characterization of a novel cryll-type gene. Appl. Environ. Microbiol. 69:5207-5211(2003). EMBL; AF111199, AAG43526.1; -- HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                 719 AA; 81024 MW; 7E17481922C435E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        96.2%; Score 3598; DB 2;
95.1%; Pred. No. 4.9e-240;
tive 23; Mismatches 12;
                                                                                          IEA
IEA
                                                                                GO; GO:0005102; F:receptor binding; IEB, GO; GO:000552; P:defense response; IEB, GO; GO:0009405; P:defense response; IEB. INTERPRO; P:GO:0009405; P:Defense response; IEB. INTERPRO; IPR00178; Endotoxin.

INTERPRO; IPR005638; endotoxin.C. INTERPRO; IPR005639; endotoxin.N. INTERPRO; IPR005639; endotoxin.N. INTERPRO; IPR008979; Gal.bind.Ike. Pfam; PF003944; Endotoxin.N; I. Pfam; PF00555; Endotoxin.N; I. Plasmid.
SEQUENCE 719 AA; 81024 MW; 7E174819
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STRAIN=BTC007;
MEDLINE=22837682; PubMed=12957903;
SONG F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
Hu Y., Li G., Huang D.,
"Identification of cryll-type genes from Bacillus thuringiensis
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MEDLINE=93298009; PubMed=8517758;
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                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein cryllc (Insecticidal delta-endotoxin
Cryll(c)) (Crystaline entomocidal protoxin) (81 kDa crystal protein)
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C18 / Egypt;
Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- FUNCTION: Promotes The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the delta endotoxin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02965; ICIY.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP03944; Endotoxin.C; 1.
Pfam; PP03945; Endotoxin.M; 1.
Pfam; PP03945; Endotoxin.M; 1.
Pfam; PP03945; Endotoxin.N; 1.
Plasmid; Sporulation; Toxin.
                                                                                                                                                                              Synonyms=cryll(c);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF056933; AAC62933.1; ~.
HSSP; P02965; 1CIY.
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33; Conservative
                                                                                                                                                  Cryl1(c)) (Crystaline e
Name=cryl1c; Synonyms=c
Bacillus thuringiensis.
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                                         GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW
                                                                                                                    361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                             VDFHWKFPTLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS
                                                                                                                                                                                                       VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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ESPICACE FROM N.A.

ESPICACIA R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AYZ62167, AAP86782.1, -.

InterPro; IPR001178; Endotoxin.

InterPro; IPR008539; endotoxin.

InterPro; IPR008539; Gal Dind INc.

InterPro; IPR008599; Gal Dind Inc.

Pfam; PF03944; Endotoxin.C; 1.

Pfam; PF03945; Endotoxin.M; 1.

Pfam; PF03945; Endotoxin.N; 1.

Pfam; PF03945; Endotoxin.N; 1.

SEQUENCE 719 AA, 81216 MM; 3627E5A6C25DAFF5 CRC64;
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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Last annotation update)
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(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
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-> Y (in strain JHCC4835 and strain HD-
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                                                                                                                  Selvapandiyan A., Bhatnagar R.K.;
Selvapandiyan A., Bhatnagar R.K.;
"Isolation, cloning and expression of cryV gene.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.
-- EVINCTION: Promotes colloidosmotic lysis by binding species.
-- EVINCTION: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
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D -> Y (in strain JHCC4835 and strain HI 1).
A -> V (in strain AB88).
KQ -> NE (in strain HD-1 and strain 61).
3627E5A6C25DAFF5 CRC64;
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thuringiensis: the cryV-encoded protein is expressed early in
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; Pred. No. 1.2e-234;
31; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                       the spore coat. MISCELLANEOUS: Toxic segment of the protein is located
                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the delta endotoxin family
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InterPro; IPR005638; endotoxin.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal. bind.like.
Pfam; PP03944; Endotoxin.C; 1.
Pfam; PP03945; Endotoxin.M; 1.
                     Mtionary phase.";
Bacteriol. 178:2141-2144(1996)
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EMBL, X62821; CAA44633.1; --
EMBL, L36339, AAC3699.1, --
EMBL, L49391, AAB00958.1, --
EMBL, X08920; CAA70124.1, --
PIR, 139815, 133815.
PIR, S25383, S55883.
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711 712 K
719 AA; 81216 MW;
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RNKALTDIKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG 180
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                                                                                              481 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
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                                                                                                                                                                                      TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAL
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; AR373207; AAK66742.1; -.
RESP; P02965; LITY.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:000405; F:pethogenesis; IEA.
GO; GO:000405; F:pathogenesis; IEA.
InterPro; IPR005639; endotoxin.C.
R InterPro; IPR005639; endotoxin.C.
R InterPro; IPR005639; endotoxin.N.
R InterPro; IPR005639; endotoxin.C.
R InterPro; IPR005639; endotoxin.C.
R InterPro; IPR005639; endotoxin.C.
R InterPro; IPR005639; endotoxin.N.
R InterPro; IPR005639; endotoxin.C; I.
R Ffam; PP03944; Endotoxin.C; I.
R Ffam; PP03955; Endotoxin.C; I.
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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92.8%; Pred. No. 2.7e-234;
ive 31; Mismatches 21;
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(TrEMBLrel. 19, I
(TrEMBLrel. 26, I
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   BEVPLLEIYAQAANLHLILIRDASIFCKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                               VDFHWKEVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
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                                                                                                 TGLNNLRGTNAKSWVRYNQFRKDWTLMVLDLVALPPSYDTLVYPIKTTSQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                               GGHRLESRPIGGALNTSTOGSTNTSINPVTLOFTSRDVYRTESLAGLNLFLTQPVNGVPR
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Spindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;

"Complete sequence of cryll gene of isolate T01 328 from Bacillus thuringiensis from Cubatao (SP - Brazil) soil.";

Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AX262167; AAP86782.1; - 3627E5A6C25DAFF5 CRC64;
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Bacillus thuringiensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=1428;
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Last sequence update)
Last annotation update)
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                                                                                                                                            Length 719;
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CACASSG4;
CACASSG4;
C2-MAR-2004 (TrEMBLrel. 27, Created)
C2-MAR-2004 (TrEMBLrel. 27, Last sequence update)
C2-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Delta-endotoxin.
CRYIA.
Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillus;
                                                                                                            719 AA; 81230 MW; 42746D478359BBA7 CRC64;
                                                                                                                                            93.9%; Score 3514; DB 2; 92.8%; Pred. No. 3.2e-234; ive 31; Mismatches 21;
InterPro, IPR005638; endotoxin_C.
InterPro, IPR005639; endotoxin_N.
InterPro, IPR008979; gal_bind_like.
Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
                                                                                                                                           Query Match
Best Local Similarity 92.8%
Matches 667; Conservative
                                                                                               Plasmid.
SEQUENCE
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                                                                                                                                                MKIKONODKHOSPSSNAKVDKISTDSLKONETDIELONINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                 RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNOYIALELMFVOKLPSFAVSG
                                                                                                                                                                                              EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
                                                                                                                                                                                                                           EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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                                                                  QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYA
     MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
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01-Nov-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Insecticidal protein.
Name-cryv101;
Bacillus thuringiensis (subsp. kurstaki).
Plasmid large plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29339;
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databases.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Zhong Q., Yuan M., Pang Y., Wan
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ dat
EMBL, ARC19593, AAC26910.1; -.
HSSP, P02955, LOTY.
GO, GO:0005102; Fireceptor binding; IEA.
GO, GO:0005922; Piedfense response; IEA.
GO, GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001178; Endotoxin.
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                                                             SEQUENCE FROM N.A.

A POTCAT M. Martinez C., Caballero P.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF278797, AAM73516.1;
PTR; B42459; B42459
HSSP; P02965, 1CIT.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:00059405; F:pedfense response; IEA.
GO; GO:0009405; P:pedfense response; IEA.
InterPro; IPR005639; endotoxin.
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R Pfam; PF03944; Endotoxin.
R Pfam; PF03945; Endotoxin.
R Pfam; PF03945; Endotoxin.N; 1.
R Pfam; PF03945; Endotoxin.N; 1.
R SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;
                       Bacillus
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                        Bacillaceae;
        Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales;
                                       NCBI_TaxID=1428;
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                                                                                           crylla-type
                                                                                                                                                                       93.9%; Score 3512; DB 2; Length 7 92.6%; Pred. No. 4.4e-234; ive 32; Mismatches 21; Indels
                                                                STRAIN=BNS3;
Tountsi S., Zouari N., Jaoua S.;
Tountsi S., Zouari N., Jaoua S.;
Tountsi and study of the expression of a novel crylla.
Bacillus thuringiensis subsp. kurstaki.";
J. Appl. Microbiol. 95:23-28 (2003).
EMBL, AJ31512; CAG659641;
EEMBL, AJ31512; CAG659641;
EEQUENCE 719 AA; 81203 MW; 8676ESA6C25DAFE8 CRC64;
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Last sequence update)
Last annotation update)
Bacillus cereus group; Bacillus thuringiensis
NCBI TaxID=29339;
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Matches 666; Conserv
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Q8KY61;
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01-OCT-2002 (
01-MAR-2004 (
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFRTIGETTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBABYDFEKAQEKV 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 AFRIVGFITPFSFSNAQSTFTIGAMNFSLGNEVYIDRIEFVFVEVTYEAEYDLKKAQDEI 660
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-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvasmot epithelial cells of many lepidopteran larvasmother.

-!- DEVELOPMENTAL STRAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
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                                                                                                                                                              301 GTVHPNASFASTTWYNNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNWW
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30-MAY-2000 (Rel. 39, Last sequence update)
50-UU-2004 (Rel. 44, Last annotation update)
50-UU-2004 (Rel. 44, Last annotation update)
65-UU-2004 (Rel. 44, Last annotation update)
67-UU-2004 (Rel. 47, Last annotation update)
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                                                          241 TGLNRLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTRMYPIPTSAQLTREVYTDAI
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                                                                                                                            GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNWW
                                                                                                                                                                                                                                                        GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR
TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI
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SEQUENCE FROM N.A.
STRAIN=NREL B-21110 / EG5847;
Donovan W.F., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins toxic to lepidopteran insects.";
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-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae. Active on Plutella xylostella and on Bombyx mori.

-!- DEVELOPMENTAL STACE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstations by European Bioinformatics institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer-
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05-UTL-2004 (Rel. 40, Last Sequence update)
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SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
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                                                                                                                               719 AA.
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Interpro; IPR005639; endotoxin.C.
Interpro; IPR005639; endotoxin.N.
Interpro; IPR008979; Gal. bind.like.
Pfam; PP03944; Endotoxin.C; 1.
Pfam; PP03945; Endotoxin.M; 1.
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                                                                                                                                   STANDARD;
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                                                                                                                               C1ID BACTU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 VPLLMVYAQAANLHLILILRDASLFGSEWGMASSDVNQYYQEQIRYTEEYSNHCVQWYNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNNLRGINAKSWVRYNOFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGT
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                         protein)
                                                                                                                         Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- PEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                            the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
             idal delta-endotoxin
(140 kDa crystal prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1233;
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                                                                     Bacillus

    -!- SIMILARITY: Belongs to the delta endotoxin family.

resticidial crystal protein crylBc (Insecticidal CrylB(c)) (Crystaline encomocidal protoxin) (140 Name=crylBc; Synonyms=crylB(c), crylBc; Bacillus thuringiensis (subsp. morrisoni).
Bacteria; Firmicutes; Bacillales; Bacillaceae; BacillaraxID=1441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.7%; Score 2459; DB 1; 364.8%; Pred. No. 6.8e-161; ive 91; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR0051378; Endotoxin.
Interpro; IPR005639; endotoxin.
Interpro; IPR008679; endotoxin N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin_0; 1.
Pfam; PF03945; Endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140451 MW;
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Best Local Similarity 64.8*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sporulation; Toxin.
SEQUENCE 1233 AA;
                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                     Gaps
                                                                                                                                                                   36;
                                                                                                                                       Length 1229;
                                                                                                                                       . Score 2459; DB 1; Length 1; Pred. No. 6.7e-161; 91; Mismatches 128; Indels
                                                   Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF0355; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
Sporulation; Toxin.
SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
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Last sequence update)
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                        IPR005639; endotoxin
IPR008979; Gal_bind_
                                                                                                                                       65.78;
                                                                                                                                                    64.8%;
                                                                                                                               Cuery Match
Best Local Similarity 64.89
Marches 470; Conservative
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Q45774;
                           InterPro;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Brizzard B.L., Whiteley H.R.;
"Nucleotide sequence of an additional crystal protein gene cloned from
Bacillus thuringiensis subsp. thuringiensis.";
Nucleic Acids Res. 16:2723-2723 (1988).
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182 QAANLHLLLIRDASLFGSEFGLTSQEIQRYYERQVERTRDYSDYCVEWYNTGLNSLRGTN
                                                                                                                                                                                                                                                                                                                                                                                      CIBA_BACTK

AC 711AA_BACTK

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AC 711A_BACTK

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 44, Last annotation update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE 6-JUL-2004 (Rel. 44, Last annotation update)

CTY1B(a) (CTYStaline entomocidal protoxin) (140 kDa crystal protein)

CTY1B(a) (CTYStaline entomocidal protoxin) (140 kDa crystal protein)

Bacillus thuringlensis (subsp. kurstaft), and

Bacillus thuringlensis (subsp. kurstaft), and

Bacillus thuringlensis (subsp. entomocidus).

CX Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                    SMAWYNNNAPSFSAIEAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPI
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                                                                              429 -TLPIASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLISASHVKAL
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-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the \ensuremath{\mathsf{N}}\xspace-
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SPECIES=B.C. entomocidus; STRAIN=HD-110;
Sociaert P.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A., STRAIN-HD-2, SPEGIES-B.t.kurstaki, STRAIN-HD-2, MEDLINE-88203216; Pubmed=3362680;
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  |:----INPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLS
                                                                                                              HIGLIIGNTLRAPVYSWTHRSADRINTIGPNRIIQIPLVKALNLHSGVTVVGGPGFTGGD
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Pred. No. 1.9e-151;
0; Mismatches 162; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINSHD-9;
Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
Submitted (Mar-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF363025; AAK51084.1; -
HSSP; P07130; IDLC.
G GO, GO.0005102; Fireceptor binding; IEA.
GO, GO.00055102; Fireceptor binding; IEA.
GO; GO.0005905; P:pathogenesis; IEA.
InterPro; IPR00178; Endotoxin.
InterPro; IPR0016538; endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR005639; endotoxin.
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InterPro; IPR006799; Gal_bind_like.
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Pfam; PF0355; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
SEOUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Delta endotoxin CrylBa2.
Name=crylBa2;
Bacillus thuringiensis (subsp. entomocidus).
Bacteria, Firmicutes; Bacillales; Bacillus.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              Query Match 62.0%; Score 2321.5; DB 1; Length 1228; Best Local Similarity 63.6%; Pred. No. 2.2e-151; Matches 453; Conservative 80; Mismatches 162; Indels 17;
                                                                                                                                                                                                                                                                                  150 150 Y -> H (in strain HD-110).
1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;
                                                                                      EMBL, X06711; CAA28988.1; -.
EMBL, X95704; CAA6503.1; -.
PIR; S00873, S00873.
HSSP, P07130; 1DLC.
INTERPO: IPR00178; Endotoxin.
INTERPO: IPR005638; endotoxin.C.
INTERPO: IPR005639; endotoxin.C.
INTERPO: IPR008979; endotoxin.N.
INTERPO: IPR008979; Gal bind like.
Pfam; PF03944; Endotoxin.C; 1.
Pfam; PF03945; Endotoxin.M; 1.
Pfam; PF03945; Endotoxin.N; 1.
Sporulation; Toxin.
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US-10-782-020-10
sequence 10, Application US/10782020
sequence 10, Application US/10782020
sequence 10, Deplication US/10782020
sequence 10, Deplication US/10782020
sequence 10, Application No. US20040197916A1
septicant: Roziel, Madine
septicant: Roziel, Michael G.
APPLICANT: Roziel, Michael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
TITLE OF INVENTION: MACHOGE for Its Use
TITLE OF INVENTION: Methods for Its Use
CURRENT APPLICATION NUMBER: US/10/782,020
CURRENT APPLICATION NUMBER: 60/448,810
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 11
scoftware: FastSEQ for Windows Version 4.0
seq ID NO ...
LENGTH: 719
twos. Ann.
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Best Local Similarity 92.9%; Pred. No. 1.4e-286;
Matches 668; Conservative 31; Mismatches 20;
7 US-10-428-961-6

7 US-10-782-141-16

7 US-10-782-141-16

7 US-10-782-141-16

8 US-10-782-570-13

3 US-10-782-570-13

3 US-10-782-570-13

4 US-10-428-961-28

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4 US-10-428-961-28

3 US-10-66-314-4

4 US-10-428-961-28

4 US-10-428-961-28

5 US-10-66-320-4

7 US-10-428-961-28

8 US-10-66-320-4

7 US-10-136-998A-2

1 US-09-988-462-13

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                                                                                                                                                                                                                                              October 28, 2004, 18:10:58; Search time 65.6795 Seconds (without alignments) 3549:224 Million cell updates/sec
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3742
1 MKLKNPDKHQSLSSNAKVDK......KRELFEIVKYAKQIHIERNM
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2: / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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4: / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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7 US-10-782-570-7
8 US-10-782-570-7
6 US-10-809-953-10
6 US-09-988-462-7
10S-09-988-462-7
8 US-10-428-961-63
1 US-09-926-660-23
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1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                            61 QTGIGIAGKILGTLGVPFAGQVASLXSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
                                                                                                                                                 121 RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
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Sequence 10, Application US/10782096;
Publication No. US20040210964A1
GENERAL INFORMATION:
APPLICANT: Carczi, Nadine
APPLICANT: Raziel, Michael G.
APPLICANT: Carc, Erian
ITLE OF INVENTION: AXM-009, A Delta-Endotoxin Gene and
ITLE OF INVENTION: AXM-009, A Delta-Endotoxin Gene and
TITLE OF INVENTION: MACHOGE for Its Use
TILE REFERENCE: 045600/274148
CURRENT APPLICANTON NUMBER: 0004-02-19
PRIOR FILING DATE: 2003-02-20
CURRENT FELING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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US-10-782-096-10
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APPLICANT: Koziel, Michael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Duck, Nicholas B.
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for its Use
TITLE OF INVENTION: Methods for its Use
TITLE OF INVENTION: Methods for its Use
TILE REFERRNCE: 045600/2143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT APPLICATION NUMBER: 06/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE PRACSEQ for Windows Version 4.0
SEQ ID NO SEGUEN MINDER: AMPLICANT MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEGEN MINDER: DELEG
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92.9%; Pred. No. 1.4e-286;
iive 31; Mismatches 20;
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Publication No. US20040197917A1
GENERAL INFORMATION:
APPLICANT: Carczzi, Nadine
APPLICANT: Hargiss, Tracy
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Best Local Similarity 92.99
Matches 668; Conservative
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US-10-782-141-8
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DB 17; Length 719; 94.1%; Score 3520; Query Match 719;

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; ORGANISM: Bacillus thuringiensis US-10-782-570-7
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Sequence 7, Application US/10782570;
publication No. US20040210965A1
GENERAL INFORMATION:
APPLICANT: Carcozi, Nadine
APPLICANT: Koziel, Michael G.
APPLICANT: Carcozi, Michael G.
APPLICANT: Carc, Brian
TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
FILE REPERENCE: 045600/274144
CURRENT FILING DATE: 2004-02-19
FRIOR APPLICATION NUMBER: 60/448,812
PRIOR APPLICATION NUMBER: 60/448,812
PRIOR PILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
           Indels
; Pred. No. 1.4e-286; 31; Mismatches 20;
  92.9%;
              668; Conservative
  Best Local Similarity
Matches 668; Conserv
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Sequence 42, Application US/10428961
Publication No. US20030237111A1
Publication No. US2003023711A1
Publication No. US2003023711A1
Publication No. US2003023711A1
Publication No. US2003023711A1
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih.Rei
APPLICANT: Donovan, William P.
APPLICANT: Rupar, Mark J.
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                                                                                                                           MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
                                                                       Gaps
                                                                    ;
                                                                       Indels
      94.1%; Score 3520; DB 17;
92.9%; Pred. No. 1.4e-286;
ive 31; Mismatches 20;
Query Match
Best Local Similarity 92.91
Matches 668; Conservative
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APPLICANT: JOOS, Henk
TITLE OF INVENTION: CEXTER HENK
TITLE OF INVENTION: CEXTER HENK
TITLE OF INVENTION: CEXTER HENK
TITLE OF INVENTION: CEXTER HENK
FILE SEPERBUCE: 021565-078
CURRENT APPLICATION NUMBER: US/10/809,953
CURRENT APPLICATION NUMBER: US/09/661,016
PRIOR PLING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: PT/EP90/00905
PRIOR PLING DATE: 1990-05-30
PRIOR PLING DATE: 1990-05-30
PRIOR FILING DATE: 1990-05-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN OF: 2.0
SOFTWARE: PATENTIN OF: 2.0
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                                                                                                                                                                                                                                                                                                                                                                            62.1%; Score 2324.5; DB 16;
63.6%; Pred. No. 9.7e-186;
iive 85; Mismatches 166; I
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Bacillus thuringiensis
      Van Mellaert, Herman
                    Botterman, Johan
Van Rie, Jeroen
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Best Local Similarity 63.67
Matches 454, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 GTVHPHPSFTSTTWYNNNAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLNRLMGNNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               710;
                                                                                                                                                                                                                                                                              9;
                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (200)..(200)
OTHER INFORMATION: The 'Xaa' at location 200 stands for any
                                                                                                                                                                                                                                           90.0%; Score 3368.5; DB 14; Length 89.2%; Pred. No. 7.2e-274; Live 32; Mismatches 37; Indels
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFWARE: Patentin version 3.2
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
                                                                                                               TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                         Best Local Similarity 89.2
Matches 641; Conservative
                                                                                                                                                                                                           US-10-428-961-42
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658 NTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

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100 QWEIFMEHVEEIINQKILTYARNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVK 159
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INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
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65.4%; Pred. No. 6.5e-185;
ive 77; Mismatches 154; Indels
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
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APPLICATION NUMBER: US 09/547,422
FILING DATE: 11.APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UNN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/72,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: S-188051 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                         Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
Death, Malnin M.
PENTICANT: Koziel, Michael G.
Kramer, Vance C.
Warren, Cregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
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Best Local Similarity 65.4
Matches 447; Conservative
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ZIP: 27709
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RESULT 7
US-09-988-462-7
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Sequence 53. Application US/10428961

Fublication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih. Rei,

APPLICANT: Chu, Chih. Rei,

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

TILE OF INVENTION: Delyancides, Compositions, and Methods of Use (Amended)

TILE OF INVENTION: Delyancides, Compositions, and Methods of Use (Amended)

TILE OF INVENTION: Delyancides, Compositions, and Methods of Use (Amended)

TILE OF INVENTION: Delyancides, Compositions, and Methods of Use (Amended)

TILE OF INVENTION WHBER: US/10/428,961

CURRENT RILING DATE: 2003-05-02

PRIOR PELING DATE: 2000-09-13

PRIOR PILING DATE: 1099-09-15

NUMBER OF SEQ ID NOS: 63

SOFFWARE: Patentin version 3.2
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160 NQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEIST 219
                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                         428 PPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRINTIGPNRITQIPMVKAS 487
                                                                                                                                                                280 TLVYPIKTTSQLTREVYTDAIGTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFL 339
                                                                                                                                                                                                                                               340 EKVTIYSLLSRWSNTQYMNMWGGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVY 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 NLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTS 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 ELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVS
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                                                                                                                                                                                                                                                                  577 INGKAINQGNFSATWNRGEDLDYKTFRTIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIBEVPVEVTYBAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFY
                                                                              FYNROVERTRDYSDHCIKWYNTGLNNLRGTNAKSWVRYNOFRKDMTLMVLDLVALFPSYD
                                                                                                                                                                                                                                                                                                                              400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFP-TLPIASDNFYYLGYAGVGTQLQDSENEL
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llarity 60.8%; Pred. No. 3.9e-178;
Conservative 100; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 LDEKRELFEIVKYAKQIHIERNM 719
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LENGTH: 1227
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US-10-428-961-63
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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23
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                                                                                                               SDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSGEEVPL 185
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                                                         IAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYARNKAL 125
                   Sequence 23, Application US/09826660

Patent No. US200100269401

GENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Narva, Kenneth E.

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1

CURRENT PILNG DATE: 1099/826,660

CURRENT APPLICATION NUMBER: US/09/826,660

FRIOR PILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1998-03-02

NUMBER OF SEQ ID NOS: 27

SOFTWARR: PARCHIN VOIT: 2.0

SOFTWARR: PARCHIN VOIT: 2.0
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ORGANISM: Artificial Sequence
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                                                                                     18;
         Length 1186;
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tch 59.3%; Score 2219; DB 9; al Similarity 60.5%; Pred. No. 6.8e-177; 432; Conservative 103; Mismatches 161;
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Bacillus thuringiensis

from

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APPLICANT: Van Rie, Jeroen
TITLE OF INVENTION: Insecticidal proteins fro
FILE REFERENCE: NEWBYTSUS2
CURRENT PEPLICATION NUMBER: US/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR APPLICATION NUMBER: 60/173387
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
SEQ ID NO 2
LENGTHARE:
                                                                                                                                                                                               TYPE: PRT ORGANISM: Bacillus thuringiensis
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                                                                                                                                                                                   Gaps
                                                                                                                                                        14; Length 1228
                                                                                                                                                                                   15;
                                                                                                                                                     58.0%; Score 2170.5; DB 14; Lengtl
60.5%; Pred. No. 8.6e-173;
.ive 98; Mismatches 171; Indels
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION WUMBER: 60/153,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 1228
                                                                                               ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38
                                                                                                                                                       Query Match
Best Local Similarity 60.5
Matches 435; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 IQSRPIGGGLNISTHGSTNISINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 OSRVHVPVYSWTHRSADRITVIISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNV
                                                                                                                                           GIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYARNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYNTGLN
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                                                                                                            12 LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLRMSEHESIDPFVSASTIQTGI
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                                                        Gaps
                                                      15;
Query Match
58.0%; Score 2170.5; DB 15; Lengt
Best Local Similarity 60.5%; Pred. No. 8.6e-173;
Matches 435; Conservative 98; Mismatches 171; Indels
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RESULT 12 US-09-826-660-25

Sequence 2, Application US/10614524
Publication No. US20040016020A1
GENERAL INFORMATION:
APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
APPLICANT: Mathieu, Eva

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Sequence 1, Application US/10089678
Sequence 1, Application US/10089678
Publication No. US20030017967A1
GENERAL INFORMATION:
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NUMBER: US/10/089,678
CURRENT APPLICATION NUMBER: US/206-05-02
PRIOR APPLICATION NUMBER: US/206-05-02
PRIOR FILING DATE: 2000-088-03
PRIOR FILING DATE: 2000-088-03
PRIOR FILING DATE: 2000-088-03
PRIOR FILING DATE: 2000-088-03
PRIOR FILING DATE: 2000-088-02
NUMBER: PRIOR FILING DATE: 2000-088-02
NUMBER: OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 YSDXCVKWYNTGLDKLKGTNAASWLKXHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LTREVYIDPIVENRETSGGFCRRWSLNSDISFSBVBSAVIRSPHLFDILSEIEFYTTRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 -RMSNTQYMMMGGHRLESRPIGGALNTSTQGSTNTSINPVT-----LQFTSRDVYRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 LPLANYTEYLEYMYGHSIKYK-----NINASSALERNYGTITSNKIKYYDLANKDIFQVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 QNYNTIDEIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLKNPDKHQSL---SSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHE----SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 IINQKILTYARNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 QKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSDHCIKWYNTGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.2%, Pre
Matches 366, Conservative 123;
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1167
TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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                                                                 APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REPERENCE: Ma-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR PILING DATE: 1998-10-23
PRIOR PILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 25
LENGTH: 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRGTNAESWLRYNOFRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDFIGRTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 IDSLKNETDI----ELKNMNN------EDYLRMSEHESIDPFVSASTIQTGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.0%; Score 1982; DB 9; Length 6
59.6%; Pred. No. 2.2e-157;
ive 94; Mismatches 148; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
COTHER INFORMATION: Toxin encoded by synthetic B.t.
US-09-826-660-25
Sequence 25, Application US/09826660 Patent No. US20010026940A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                       APPLICANT: Cardineau, Guy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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530 INRNNGNIQNRGYIEVPIQFTSTSTRYRVRVRYRASVTSIELNVNLGNSSIFTNTLPATAA
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                                                            538 -RTNTGTF---GDIRVNIN-PPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 IDPFVSASTIQTGIGIAGKILGTLGVPFAGQIASLYSFILGELWP-KGKSQWEIFWEHVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PETFISSSTIQTGIGIVGRILGALGVPFASQIASFYSFIVGQLMPSKSVDIMGEIMERVE
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                                                                                                                                   RGEDLDYKTFRTIGFTTPPSFSDVQSTFT-----IGAWNFSSGNEVYIDRIEFVPVEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
44.3%; Score 1657.5; DB 17; Lengt
Best Local Similarity 48.9%; Pred. No. 1e-129;
Matches 368; Conservative 107; Mismatches 228; Indels
                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/10782141

| Publication to US2004019791741
| Publication to US2004019791741
| GENERAL INFORMATION:
| APPLICANT: Carcozzi, Nadine
| APPLICANT: Raziel, Michael G.
| APPLICANT: Carc, Nicholas B.
| APPLICANT: Carr, Brian
| TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and TITLE OF INVENTION: AXMI-0143
| TITLE OF INVENTION: Methods for Its Use
| FILE REPREADED: 045600/274443
| CURRENT FILING DATE: 2004-02-20
| PRIOR APPLICATION NUMBER: 60/448,632
| PRIOR FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ 1D NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 1D NO 16
LENGTH: 1157
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-782-141-16
                                                                                                                                                                                                           647 YEAEYDFEKAQE 658
                                                                                                                                                                                                                            :| ||| |:||:
641 FEVEYDLERAQK 652
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US-10-782-141-16
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JOHNSTAND LAND, CALLARE A.

JAPPLICANT: Chu, Chih-Rei

APPLICANT: Chu, Chih-Rei

APPLICANT: Gluer, William P.

APPLICANT: Gluer, Mark J.

APPLICANT: Gluer, Mark J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: DAPPLICATION WUMBER: 109/661,322

FRIOR FILING DATE: 2000-09-13

FRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 6
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                           70 ILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYARNKALSDLR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ILGVLGVPFAGQLASFYSFLVGELMPSGRDPWEIFLEYVEQLIRQQVTENTRNTAIARLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGTVHPNQAF 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 SSNAKVDKIATDSLKN---ETDIELKNMNNEDYLRMSEHESIDPFVSASTIQTGIAGK
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       FIIGAWNFSSGNEVYIDRIBFVPVEVTYBABYDFBKAQEKVTALFISTNPRGLKTDVKDY
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llarity 51.3%; Pred. No. 2.8e-132;
Conservative 111; Mismatches 169; Indels
                                                                             680 HIDOVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719
                                                                                                  RESULT 14
US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US2003037111A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Matches 345;
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70S VECLSDDLYPNEKRLIFDAVREAKRLSGARNL 736	Оb
688 VESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719	ò
QDLEAAKKAVNALFTNTKD-GLRPGVTDY	ДC
628 SSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNL 687	ò
ASI	dC
568 TIDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFRIIGFTTPFSFSDVQSTFTIGANNF 627	ò
PGFTC	đ
508 TQIPLVKAFNLSSGAAVVRGPGPTGGDIRRTNTGTFGDIRVNINPPFAQRYRVRIRYAS 567	Š
470 IPLDRI-VPVAESYSHRLSHITSHSFSKNGSAYYGSFPVFVWTHTSADLNNTIYSDKI 526	qq
456 LPPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSI 507	ò
415 STVANLANYQKAYGVPGSWFHWVRRGTSSTTAYL-YSKTHTALQGGTQVYESSDE 469	qq
403 SLAGINLFLTQPVNGVPRVDFHW-KFPTLPIASDNFYYLGYAGYGTQLQDSENE 455	δ

Search completed: October 28, 2004, 18:41:13 Job time : 68.6795 secs

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The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66911 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant
Aar54074
Aaw35259
Aaw87623
Aay30923
Aar50953
Aar50955
Aau02094
Aaw44321
Aaw44321
Aaw44321
Aaw44321
Aaw44321
Aaw46204
Aaw46204
Aaw16795
Aaw10679
Aaw16796
Aaw00420
Aaw8628
Aaw00420
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llarity 100.0%; Pred. No. 2e-300;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insecticide; transgenic plant; insect-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mackay EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                            AAX31990
AAW44321
AAU02046
AAW44322
AAW19947
AAW100421
AAU00420
AAU00420
AAU00420
AAW84628
AAW84628
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AAU02094
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                                                                                                                                                                                                                                                                 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
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            MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIBLKNMNNEDYLRMSEHESIDPFVSASTI
                                QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYA
                                                                                                                                                                                                GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pesticide; insecticidal crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. thuringiensis insecticidal crystal endotoxin (CRY)
                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 719
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal artivity. The present sequence is sequence is used in the invention
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protein comprising an X-glycine motif as an active ingredient of a pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 3742; DB 6; Best Local Similarity 100.0%; Pred. No. 2e-300; Matches 719; Conservative 0; Mismatches 0;
                                                                                    Claim 12; Page 56-58; 67pp; English
  New insecticidal terminus, useful
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 719 AA;
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719

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The present sequence represents the Bacillus thuringiensis (Bt) isolate C -18 (BtC-18) crystal II (Cryll) protein. Bt is a bacterium which produces crystalline inclusions during sporulation, composed primarily of a single polypeptide. These crystal proteins (Cry. e.g. class Cryl) exhibit highly specific insecticidal activity, so that most Bt strains kill insects belonging to only one order. The invention claims for a stable BtC-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis isolate C-18; BtC-18; Bt; crystal 11; Cryl1; sporulation; insecticidal activity; pest control; rootworm; agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity
isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis isolate C-18 crystal 11 protein.
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(MADK/) MADKOUR M.
(BULL/) BULLA L A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel Bacillus thuringiensis cryl gene, gene combination, expression vector, nucleotide sequence of the B thuringiensis cryl gene with high-texicity to lepidoptera pests and the amino acid sequence of the protein encoded by it, cooperative use of the cryl gene with the expression product of crylab or crylBa, primer sequences for expressing the genes, and the constructed shuttle vector pSX422b. The gene in combination with the crylab or crylBa genes displays high toxicity to the lepidoptera, coleoptera and diptera pests. The present sequence represents the cryllel protein.
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                                                                                                                                                                                                                                                          toxicity; lepidoptera; crylAb; crylBa; coleoptera; diptera;
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95.1%; Pred. No. 1.7e-288;
ive 23; Mismatches 12;
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                                                                           protein; 719
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684; Conservative
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N-PSDB; ADM74716.
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strain which produces at least three different types of crystal proteins and is therefore claimed to be capable of killing insects from at least three orders, thus providing a sultable alternative for broad-spectrum agricultural pest control. The isolated crystal proteins, for e.g. other insecticidal proteins and is useful to produce antibodies to other similar proteins from other strains/ organisms. The invention also provides a BCC-18 toxin protein which is active against roctworms. The Cry encoding nucleic acids are claimed to be useful for expressing the Cry proteins in plants, to produce pest-resistant transgenic plants and plant products, or in micro-orans, which can be applied to protect agricultural crops. They are also useful to isolate mucleic acids encoding potentially pesticidal proteins from other strains/organisms by
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95.0%; Pred. No. 3.4e-284;
iive 11; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                   of Paecilomyces
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                                                                                                                                                                                                                                                                                                                                                                          Novel insecticidal protein obtained from species of Paecilomycontrolling insects, and for insect-resistant transgenic plant production.
                                                                                                                                                                                                                                                                                                               Warner SAJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 719;
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                                                                                                Insecticide; transgenic plant; insect-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.1%; Score 3520; DB 4;
92.9%; Pred. No. 4.8e-282;
tive 31; Mismatches 20;
                                                                                                                                                                                                                                                                                                               Mackay EA,
                                                                                                                                                                                                                                                                                                               Cayley PJ,
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                                                                                                                                                                                                              23-JUN-2000; 2000WO-GB002457.
                                                                                                                                                                                                                                         99GB-00015215.
                                        (first entry)
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                                                                                                                                                                                                                                                                                                             Carlile AJ,
                                                                     protein
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                                                                                                                           Paecilomyces sp
                                                                                                                                                      WO200100841-A1.
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23-DEC-1999;
                                                                     Insecticidal
                                        12-APR-2001
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Vincent JL,
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Matches 668;
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> AAB66908 standard, protein; 719 RESULT 5 AAB66908 ID AAB6

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QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEBIINQKISTYA
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                                                                                                       EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYA
                                             RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
                                                                                                                                          TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI
                                                                                                                                                      GTVHPNQAFASTTWYNNNAPSFSAIBAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMW
                                                                                                                                                                                                                                     GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR
                                                                                                                                                                                                                                                            361 GGHKLEFRTIGGILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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99GB-00030536.
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Lee MD;
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23-DEC-1999;
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               480
                                      540
                                                  ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
                                                                                   TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
                                                                                                 TFRTIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYZAEYDFEKAQEKV 660
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     UDEHWKEVTHPIASDNPYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS
                                      ASHVXALVYSWTHRSADRTNTIEPNSITQIPLVXAFNLSSGAAVVRGPGFTGGDILRRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
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                                                                                                                                                                                                                                                                                                                                        endotoxin (CRY)
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                                                                                                                                                                                                                                                                                                                                        crystal
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                                                                                                                                                                                                                                                                                                                                        thuringiensis insecticidal
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                                                                                                                                                                                                                                                                   standard; protein;
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Matches 668; Conserv
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(first entry)

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Insecticidal protein; pesticide; insecticidal crystal endotoxin;
                                                         thuringiensis insecticidal crystal endotoxin (CRY)
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                                                                                                    The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are linsect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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                                    for
                                   protein obtained from species of Paecilomyces
                                                                                                                                                                                                                           ;
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                                 Novel insecticidal protein obtained from species of Paecilomyc controlling insects, and for insect-resistant transgenic plant
                                                                                                                                                                                                 Length 719;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                   Score 3516; DB 4;
Pred. No. 1e-281;
l; Mismatches 21;
                                                                                72pp; English
                                                                                                                                                                                            94.0%; Scor
92.8%; Pred
                                                                                                                                                                                                              Best Local Similarity 92.8
Matches 667; Conservative
                                                                               Claim 14; Page 60-62;
            WPI; 2001-123015/13
                                                                                                                                                                           Sequence 719 AA;
                                                        production
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RESULT 8 AAE36274 ID AAE36274 standard; protein; 719

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                                                                                                                                                                                                                                                                                                                                                                                                                       motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The producing plants or plant parts that are an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
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                                                                                                                                                                                                                                                                                                                                       New insecticidal protein comprising an X-glycine motif a terminus, useful as an active ingredient of a pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%; Score 3516; DB 6; 92.8%; Pred. No. 1e-281; ive 31; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 50-53; 67pp; English
                                                                                                                          30-MAY-2002; 2002WO-GB002666.
                                                                                                                                                                  07-JUN-2001; 2001GB-00013900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tches 667; Conservative
Bacillus thuringiensis
                                                                                                                                                                                                                                                     Vincent JL, Viner R;
                                                                                                                                                                                                             (SYGN ) SYNGENTA LID
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Best Local Similarity
Matches 647.
                                                                                                                                                                                                                                                                                                                                                           terminus, useful
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                                                                                  12-DEC-2002
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                                     Score 3511; DB 4;
Pred. No. 2.7e-281;
                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB66911 standard; protein; 719
                                         93.8%;
92.8%;
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                                                                                   Conservative
                                                             Similarity
  AA;
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Sequence 719
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                                         Query Match
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AAB66911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                               540
                                                                                                                                                                                        009
                                                                                                         540
                                                                                                                                                                                                                 TGTFGDIEVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYK 600
                                                                                                                                                                                                                                                                        TERTIGETTPESFSDVOSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYBAEYDFBKAQEKV 660
                                                                                                                                                                                                                                                                                                  TERTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Crylla; CrylBa; moth; butterfly; Colorado potato beetle;
mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is B. thuringiensis (Bt) crystal protein Crylla, the DNA encoding which was mutated to allow cloning of domain III or domains I and II, to make the hybrid protoxins of the invention. The hybrid toxins of the invention, having structural domains I, II and III in this order starting from the N-terminal derived from at least 2 different crystal proteins, are useful for protecting plants against pest insects, e.g. moths, butterflies and Colorado potato beetle or for combating insects
                                                                                                                                                                                                                                                                                                                                                       TALFISINPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM 719
                                                                                                                                                                                                                                                                                                                                                                               VDFHWKFPTLP1ASDNFYYLGYAGVGTQLQDSENELPPETTGQPNYESYSHRLSH1GL1S
                                                  ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                        TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
                                                                                                       ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis partial mutant Crylla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20. .719
/label= Mature_Crylla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02095 standard; protein; 719
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Peptide
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The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNKALTDIKGLGDALAVYHDSLESWVGNRNNTRARSVVRSQYIALELMFVQKLPSFAVSG 180
                                         661 TALFTSTWPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM 719
                                                                                                                                                                                                                                                   thuringiensis insecticidal crystal endotoxin (CRY) protein, crylla5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIINQKISTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEVPLLPIXAQAANLHILLIRDASI FGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLNNLRGTNAKSWVRYNQFRKDWTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHEDCLKMSEYENVEPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
                    TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                       Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at the amino-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insecticidal protein comprising an X-glycine motif a terminus, useful as an active ingredient of a pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 3509; DB 6; 92.5%; Pred. No. 3.9e-281; ive 33; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 53-56; 67pp; English
                                                                                                                                               Ā
                                                                                                                                               AAE36275 standard; protein; 719
                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2002; 2002WO-GB002666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2001; 2001GB-00013900.
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 665; Conservative
                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vincent JL, Viner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYGN ) SYNGENTA LTD
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                                                                                                                                                                                 AAE36275;
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                                                                                                                                                                                                                                                                                                                   The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVBEIINQKILTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEVPLIPIYAQAANLHLLLIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGLNNLRGTNAESWVRYNOFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK
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                                                                                                                                                                                                    Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.
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                                                                                                                            Warner SAJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 3509; DB 4; 92.5%; Pred. No. 3.9e-281; iive 33; Mismatches 21;
                                                                                                                          Mackay EA,
                                                                                                                          Cayley PJ,
                                                                                                                                                                                                                                                                                     Claim 14; Page 62-64; 72pp; English
                                 99GB-00015215.
 2000WO-GB002457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 92.5
les 665; Conservative
                                                                                                                          Carlile AJ,
Lee MD;
                                                                                                                                                                               WPI; 2001-123015/13
                                                                                      (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 719 AA;
23-JUN-2000;
                                   29-JUN-1999;
23-DEC-1999;
                                                                                                                          Griffin J,
Vincent JL,
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                                                                                                                                                                                                                                                                                                                 241 IGLANLRGTNAESWVRYNQFRRDWTLMVLDLVALPPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTVHPNOAFASTTWYNNNAPSFSALEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMW
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                                                                                                                                                  QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFWEHVEEIINQKILTYA
                                                                                                                                                                                                                                       QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA
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                                                                                                                         1 MKLKNPDXHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                  EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; pesticide; insecticidal crystal endotoxin;
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                                                                                   Indels
                                        Length
                                      93.6%; Score 3503; DB 4; 92.5%; Pred. No. 1.2e-280; ive 32; Mismatches 22;
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                                        Query Match
Best Local Similarity
Matches 665; Conserv
  Sequence 719 AA;
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                                                                 GTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWW
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TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
                                                                                                                             GCHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                          GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMW
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The sequence carried on pJH12 which was isolated from B. thurin- giensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E.coli strain NC12022/DH12 (NCIB 40279) or bacteriophage EMB4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.
601 TFRIVGFITPFSFLDVQSTPTIGAMNFSSGNEVYIDRIEFVPVEVTYEAEYDFEKAQEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 EEVPLLPIYAQAANLHLLLIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFWEHVEEIINQKILTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMMNEDYLRMSEHESIDPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | MXLKNOKHQSFSSNAKVDKLSTDSLKNETDIELQNINHEDCLKNSEYENVEFFVSAST
                                                                          661 TALFISTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3499; DB 2;
Pred. No. 2.7e-280;
                                                                                                                                                                                                                                                                                                                                                                                                                     Crystal; insecticide; toxin; delta endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis; JHCC 4353 and 4835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tippett JM;
                                                                                                                                                                                                                                                                                                                                                                             DNA carried
                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 5-10; 66pp; English
                                                                                                                                                                                                    AAR08041 standard; protein; 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                           kD endotoxin deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.5%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89GB-00010624.
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                                                                                                                                                                                                                                                                                        (revised)
(revised)
(first entry)
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Matches 665; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1990-361486/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 719 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-1989;
                                                                                                                                                                                                                                                                                     24-OCT-2003
25-MAR-2003
27-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9013651-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RG,
                                                                                                                                                                                                                                              AAR08041;
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Best Local S
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                                                                                                                                                                                                                                                                                                               motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALBLMFVQKLPSFAVSG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MXLKNPDKHQSLSSNAKVDK1ATDSLKNETD1ELKNMNNEDYLRMSEHESIDPFVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                         at the amino-
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                         New insecticidal protein comprising an X-glycine motif a terminus, useful as an active ingredient of a pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 3503; DB 6;
Pred. No. 1.2e-280;
2; Mismatches 22;
                                                                                                                                                                                                                                                                                          Claim 12; Page 47-50; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.6%; Sco
92.5%; Pre
tive 32;
                                                  07-JUN-2001; 2001GB-00013900
      30-MAY-2002; 2002WO-GB002666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.5
Matches 665; Conservative
                                                                                          (SYGN ) SYNGENTA LTD
                                                                                                                                                                                  WPI; 2003-175137/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         719 AA;
                                                                                                                                      Vincent JL,
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other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. sequence is used in the invention

Sequence 718 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify
                                                                                                                                                                             ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRIN
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                         TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI
                                                                                                             GGHRLESRPIGGALNTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPR
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           TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI
                                                           GTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMW
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Sequence 9, Ai
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Sequence 8, A
Sequence 42,
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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US-08-257-999-2
US-08-257-999-2
US-08-325-547-5
US-08-379-656B-5
US-08-379-656B-5
US-08-379-656B-5
US-08-1177-5
US-09-471-177-5
US-09-471-177-5
US-09-210-806-5
US-08-210-806-5
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US-08-210-806-5
US-08-210-806-5
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Sequence 2, Application US/09003217
Patent No. 5986177
GENERAL INFORMATION:
APPLICANT: Osman, Yehia A.
APPLICANT: MadXcur, Maddy A.
APPLICANT: BALIA, Lee A.
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.8%; Score 3546; DB 2; 95.0%; Pred. No. 5.6e-318; ive 11; Mismatches 25;
                                                                                                                                                                                                                                                 E: W. Murray Spruill (Alston & Bird, 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGIGSTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELEPHONE: 919 420 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
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MOLECULE TYPE: protein

US-09-003-217-2
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CLASSIFICATION: 800
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COUNTRY:
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; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENEMAL INFORMATION:
APPLICANT: OSMAN, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
TITLE OF INVENTION: Activity
; FILE REFERENCE: CTVI
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; BALLIER PLING DATE: 1998-01-06
; WUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
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                                                    RNKALSDIRGIGDALAVYHESIESWVENRNTRARSVVKNQXIALEIMFVQKIPSFAVSG
                                                                   RNKALTDLKGLGDALAVYHESLESWVGNRNNTRARSVVKNQYTALELMFVQKLPSFAVSG
                                                                                                     BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYN
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94.6%; Score 3541; DB 3; Length 719;
Best Local Similarity 95.0%; Pred. No. 1.5e-317;
Matches 683; Conservative 11; Mismatches 25; Indels
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1 WKLKNPDKHQTLSSNAKVDKIATDSLKNFTDIELKNMNBDYLRMSEHBSIDPFVSASTI
                                                                       QTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIINQKILTYA
                                                                                                                                                          RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Sequence 8, Application US/08286870A

Sequence 8, Coffice
GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TIPPETT, JM
APPLICANT: TIPPETT, JM
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN
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FEATURE:
NAME/KEY: misc_feature
NAME/KEY: (200)
LOCATION: (200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42
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ORGANISM: Bacillus thuringiensis
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US-09-661-322A-42
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILLING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/52028
FILLING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U6 99
ATTORNEY/AGENT INFORMATION:
NAME: PALJ N. KOKUJIS
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 70608/220720
TELEPHONE: (202) 821-3000
TELEPHONE: (202) 821-3000
TELEPHONE: (202) 822-0944
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TOTAL AND ACCUSED SECONDAL AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED AND ACCUSED SECONDAL ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSE
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Best Local Similarity 92.8
Matches 667; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
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GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Composi;
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42
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                         661 TALPTSINPRGLKTDVQDYHIDQVSNLVESLSDEFYLDEKRELFELVKYAKQLHIERNM 719
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90.0%; Score 3368.5; DB 4;
Best Local Similarity 89.2%; Pred. No. 1.2e-301;
Matches 641; Conservative 32; Mismatches 37;
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300 300 360 360 420 420 480 480 540

180 240

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RNKALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSG
                                                   121 RNKALTDLKGLGDALAVYHDSLESWVGNRNNTRARSVVKSQYIALELMFVQKLPSFAVSG
                                                                                                           181 BEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKMYN
                                                                                                                                         241 TGLNNLRGTNAESWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTDAI
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ZIF: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PC-DOS/MS-DOS
MEDIUM SYSTEM: PC-DOS/MS-DOS
MEDIUM SYSTEM: PC-DOS/MS-DOS
MEDIUM SYSTEM: PC-DOS/MS-DOS
MEDIUM SYSTEM: PC-DOS/MS-DOS
MEDIUM SYSTEM: NOWBER: US/08/286,870A
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
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Patent No. 6063605
GENERAL INFORMATION:
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TAILOR, RH
APPLICANT: TAILOR, RA
APPLICANT: TAILOR, RA
APPLICANT: TAILOR, RA
APPLICANT: TAILOR, RA
APPLICANT: TAILOR, RA
APPLICANT: ADEREX: RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORESSPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-08-286-870A-6
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TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 591
                                                                  601 TERTIGETTPESFSDVQSTFTIGAMNESSGNEVYIDRIEFVPVEVTYEARYDFEKAQEKV 660
                                                                                                  592 TPRIVGFTIPPSFSDVQSTFIIGAMNFSSGNEVXIDRIEFVPVEVIYEAEYDFEKAQEEV 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISW PC Compatible
COMPUTER: ISW PC Compatible
COMPUTER: PREADABLE
SOFFWARE: PACENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AM4-1994
CLASSIFCATION: 435
PRIOR APPLICATION NUMBER: US 07/52028
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
NAME: PAUL N. KOKULIS
NAME: PAUL N. KOKULIS
NAME: PAUL N. KOKULIS
NAME: PAUL N. KOKULIS
NAME: PAUL N. KOKULIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN DARBY & CUSHMAN ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70608/220720
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APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
ITTLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        RESULT 5
US-08-286-870A-4
Sequence 4, Application US/08286870A
; Patent No. 6063865
; Patent No. FURNATION:
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REFERENCE/DOCKET NUMBER: 7060
TELECOMMULCATION INFORMATION: TELEPHONE: (202) 861-3000
TELEFAX: (202) 821-9944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 648 amino acids
amino acid
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Best Local Similarity 92.3$
Matches 598; Conservative
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299 TNAPSGFASTNWFNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 INNLRGTNAESWLRYNOFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |::----INPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VPLLMVYAQAANLHLILLRDASIFGSEWGMASSDVNQYYQEQIRYTEEYSNHCVQWYNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 LNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 VHPNQAFASTIWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNMWGG
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                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APENICATION DATA:

PFILING DATE: 1930729

FLING DATE: 1930729

FLING DATE: 1930729

TLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: EGGL, Christopher:

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 75034

TELECHOMUNICATION INFORMATION:

TELECHOMUNICATION INFORMATION:

TELECHOMUNICATION INFORMATION:

TELECHOMUNICATION INFORMATION:

TELECHOMUNICATION INFORMATION:

TELECHOMUS: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

TANGEMENT ILZ29 amino acids
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TOPOLOGY: linear
TedH,E TYPE: protein
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Best Local Similarity
Matches 470; Conserv
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Patent No. 532267
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panich Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTGIGIAGKILGTLGVPFAGQVASLYSFILGELWPKGKNQWEIFWEHVEEIINQKISTYA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEVPLLPIYAQAANIHLILIRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI
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                                                                                                                                                                                                                                                                                                                                                        Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                        tch 68.8%; Score 2573; DB 3; al Similarity 91.0%; Pred. No. 1.9e-228; 487; Conservative 29; Mismatches 19;
                                                                            70608/220720
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFRA: (202) 861-3000
TELEFRA: (202) 862-0944
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-286-870A-6
                                                                                                                                                                                                                                                                 linear
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Best Local S
Matches 487
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Sequence 4, Application US/08474038
Sequence 4, Application US/08474038
Batent No. 5679343
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
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                                                                                                                             239 INNIRGTNAESWIRYNQFRRDLIGVLDLVALFPSYDTRTYPINTSAQLTREIYTDFIGR
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                                                                                                                                                                                                               303 VHPNQAFASTIWYNNNAPSFSAIBAAVIRSPHLLDFLEKVTIYSLLSRWSNIQYMNWWGG
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CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/474,038
FILING DATE: 07-JUN-1995
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CITY: Philadelphia
STATE: Pennsylvania
COUMTRY: U.S.A.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,865
"TITING DATE: 30-DEC-1993
"TITING DATE: "TITING DATE: US 08/100,709
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
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                                        KAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIH 714
                                                                                              652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEKVKYAKRLS 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-DEC 1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 20-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08176865 Patent No. 5616319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-757-1590 INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 64.84
Matches 470; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 KALSDIRGIGDALAVYHESIESWVENNNTRARSVVKNOYIALELMFVOKLPSFAVSGEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 VHPNQAFASTTWYNNNAPSFSAJEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMWGG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 TNAPSGFASTNWFNNNAPSFSAIZAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYWVG 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 RFNF-----INPONIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLS 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1229;
                                                                                                                                                                                                                                                                                                                                                                                                                                        65.7%; Score 2459; DB 1; Length 1 64.8%; Pred. No. 2.5e-217; ive 91; Mismatches 128; Indels
FILING DATE: 29-JULLICO.

ATTORNEY/AGENT INFORMATION:

NAME: EGOLf, Christopher

REGISTRATION NUMBER: 2763

REFERENCE/DOCKET 1705-49

TELEPONNINICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPONE: 215-75-11590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

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Best Local Similarity 64.8
Matches 470; Conservative
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APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Ganzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYET4 AND CTYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSE: Addel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STREET: Philadelphia
STREET: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 VPLLMVYAQAANLHLLLLRDASLFGSEWGMASSDVNQYYQGQIRYTEEYSNHCVQWYNTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTIQT
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64.8%; Pred. No. 2.5e-217;
ive 91; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-UUL-1993
ATTORNBY/AGENT INFORMATION:
NAME: EGOLF, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 72634
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
Sequence 4, Application US/08779046
Patent No. 5854053
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.8<sup>3</sup>
Matches 470; Conservative
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MOLECULE TYPE: protein
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298

534 532 594 592 654

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243 INNIRGINAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGT 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 KAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIH 714
                                                                                                                                                         63 GIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKSQWBIFMEHVEBLINQKILTVARN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRLESRPIGGALNTSTQGST-NTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPRV 421
                                                                                        3 LKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNWNNEDYLRMSEHESIDPFVSASTIQT
                                                                                                                  59 GINIAGRILGVLGVPFAGQLASFYSFLVGELWPSGRDFWEIFLEHVEQLIRQQVTENTRN
                                                                                                                                                                                                                                                239 IANNEGTNABSWERYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 BDLDYKIFRIIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVTYSAEYDFE
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652 RAQKAVNALFISTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEKVEKYAKRLS
                                                                                                                                                                                                                                123 KALSDLRGLGDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSFAVSGEE
                                                                                                                                                                                                                                                                                                 VPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSDHCIKWYNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 DEHWKFPTLPIASDNFYYLG-----YAGVGTQLQDSENELPPETTGQPNYESYSHRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 RFNF-----INPONIYERGATTYSOPYOGVGIQLFDSETELPPETTERPNYESYSHRLS
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                         Length 1229;
                         ; Score 2459; DB 2; Length 1; Pred. No. 2.5e-217; 91; Mismatches 128; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ROZiel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
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APPLICANT: Kramer, Vance C.
APPLICANT: Kramer, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Cossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
                            65.7%;
64.8%;
                                               Best Local Similarity 64.8 Matches 470; Conservative
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                                             Similarity
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US-07-951-715A-7
US-08-881-340-4
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                              Query Match
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Patent No. 5942658

GENERAL INFORMATION:
APPLICANT: Dany, William P.
APPLICANT: Tan, Yuging
APPLICANT: Tan, Yuging
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYET4 AND CTYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
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HRLESRPIGGALNISTOGST-NISINPVILOFISRDVYRTESLAGINLFLTQPVNGVPRV 421
                   -YAGVGTOLODSENELPPETTGOPNYESYSHRLS
                                                                                                   RFNF-----INPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLS
                                                                                                                                     HIGLISASHVKALVYSWTHRSADRTNTIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD
                                                                                                                                                                                                     ILRRINIGIFGDIRVNINPPFAQRYRVRIRYASTIDLQFHISINGKAINQGNFSATMNRG
                                                                                                                                                                                                                                                                      EDLDYKTFRTIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYIÖRIBFVPVEVTYEAEYDFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,340

FLING DATE: 24-JUN-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/100,709

FLING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: BG01k, Christopher:

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7265-49

TELEPHONE: 215-75-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    DFHWKFPTLPIASDNFYYLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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US-08-881-340-4
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368 RIESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDRGTANYSQPYESPGLQLKDSBIEL 427
                                                                               457 PPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAF 516
                                                                                                                                                                                                                                                                                                              637 RIBFVPVEVTYBABYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFY 696
                                                                                                                                                                                                                                                                                                                                                                                                              428 PPETTERPNYESYSHRLSHIGIILQSRVNVPVYSWTHRSADRINTIGPNRITQIPMVKAS
                                                                                                                                                                                                                               488 ELPQGTTVVRGPGPTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFFVS
                                                                                                                                                                               517 NLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAORYRVRIRYASTTDLOFHTS
                                                                                                                                                                                                                                                                              577 INGKAINQGNFSATMARGEDLDYKTFRTIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marie, Nation of APPLICANT: Warren, Vance C. APPLICANT: Warren, Gregory W. APPLICANT: Warren, Gregory W. APPLICANT: Broad, Lyle D. APPLICANT: Wright, Martha S. APPLICANT: Wright, Martha S. APPLICANT: Marthin, Blis J. APPLICANT: Bowman, Cindy G. APPLICANT: Bowman, Cindy G. APPLICANT: Dawson, John L. APPLICANT: Dawson, John L. APPLICANT: Dawson, Sharren L. APPLICANT: Bay, M. APPLICANT: Bay, M. APPLICANT: Suttie, Janet L. TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHALTILE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE MARIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
STRESPONDENCE NO. 555936artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
GITY: Tarrytown
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-5EP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 LDEKRELFEIVKYAKQIHIERNM 719
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Desai, Nalini M.
Lewis, Kelly S.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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2
APPLICANT: Launis, Karen L.
APPLICANT: Rochstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Duder, Erik M.
APPLICANT: Punder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Rutie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: SINVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INBECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 61.9%; Score 2314.5; DB 1; Length al Similarity 65.4%; Pred. No. 5.3e-204; 447; Conservative 77; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-58P-1992
CLASSIFICATION NUMBER: US 07/772,027
FILING DATE: 04-007-1991
APPLICATION NUMBER: US 07/772,027
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REFERENCE/DOCKET NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive CITY: Hawthorne STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10532
COMPUTER REAABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: (319)541-8615
TELEFAX: (319)541-8615
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 ami-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local S
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                  130 TQYIALELDFINAMPLFAIRNQEVPLLMVYAQAANLHLLLIRDASIFGSEFGITSQEIQR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYNRQVERTRDYSDHCIKWYNTGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLVYPIKTISQLTREVYTDAIGTVHPNQAFASTTWYNNNAPSFSAIEAAVIRSPHLLDFL 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 RGGTTVMNFRFLRTMNSGDELKYGNFVRRAFTTPFTFTQIQDIIRTSIQGLSGNGEVYID 607
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                                                                                                                                                                                                                                                                                    40 EDYLRMSEHESIDPFVSASTIQTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 NLSSGAAVVRGPGFTGGDILRRINTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTESLAGINLF -- LTQPVNGVPRVDFHWKFP-TLPIASDNFYYLGYAGVGTQLQDSENEL
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                        DB 2; Length 1207;
                                                                                                                                                                                                      Query Match ,61.9%; Score 2314.5; DB 2; Length Best Local Similarity 65.4%; Pred. No. 5.3e-204; Matches 447; Conservative 77; Mismatches 154; Indels
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: GG 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8589
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH : 1207 anino acids
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: protein
                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-08-459-595A-7
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Sequence 7, Application US/08459595A Patent No. 60181.04 GENERAL INFORMATION: APPLICANT: Koziel, Michael G. APPLICANT: Desai, Nalini M:

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220 FYNROVERTRDYSDHCIKWYNTGLNNLRGTNAKSWYRYNQFRKDMTLMVLDLVALFPSYD 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 EDYLRMSEHESIDPFVSASTIQTGIGIAGKILGTLGVPFAGQIASLYSFILGELWPKGKS
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65.4%; Pred. No. 5.3e-204;
tive 77; Mismatches 154; Indels 5;
                                                                                                                                                                                                                                                       ENHANCED
                                                                                                                                                                                                                                                            STREET: Rd., POB 2005
CITY: Tarrytown STREET: New York
COUNTRY: Usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
FILING DATE: US/08/459,595A
ATPOINT INFORMATION:
NAME: Pace, GATY M:
REGISTRATION NUMBER: US/07/72,027
FILING DATE: US/08/459A
ATPOINT INFORMATION:
NAME: Pace, GATY M:
REGISTRATION NUMBER: CGC 1577/CIP/DIV3
TELECHOME: (919)541.8582
                                                                                                                                                                APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING E TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           Rothstein, Steven J.
Bowman, Cindy G.
                                      Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Gregory
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Best Local Similarity 65.4%
Matches 447; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-459-595A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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130 TQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQR 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 EDSLCIAEGUNIDPFVSASTVQTGINIAGRILGVLGVLGVFAGQLASFYSFLVGELWPRGRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 NQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLLRDASIFGKEWGLSASEIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.9%; Score 2314.5; DB 3; Length
65.4%; Pred. No. 5.3e-204;
ive 77; Mismatches 154; Indels
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                                                                                              UMBER: US 07/951,715
25-SEP-1992
                                                               US 08/459,595
                                                                                                                                                                  US 07/772,027
                                                                             FILING DATE: 02-UN-195
APPLICATION NUMBER: US 07/951
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772
FILING DATE: 04-0CT-1991
ATTONEY/AGENT INFORMATION:
NAME: Mediss, J. Timochy
REGISTRATION NUMBER: 38, 241
REGISTRATION NUMBER: 38, 241
REGISCOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                               TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 1207 amino acids
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Best Local Similarity 65.49
Matches 447; Conservative
                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                               637 RIBEVPVEVTYBAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFY 696
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                                         TLVYPIKTISQLIREVYIDAIGTVHPNQAFASTIWYNNNAPSFSAIBAAVIRSPHLLDFL 339
                                                                          250 TRIYPINTSAQLTREVYTDAIGATGVN--MASMNWYNNNAPSFSAIEAAAIRSPHLLDFL 307
                                                                                                                                                                                                                                                                                                                                                                                                   ELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVS
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                                                                                                                                                                                                                                                                                                                                                                         517 NLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 INGKAINQGNESATWNRGEDLDYKTFRTIGFTTPFSFSDVQSTFTIGAWNFSSGNEVYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Roziel, Michael G.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Warren, Gregory W.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Rothstein, Steven J.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Clindy G.
APPLICANT: Bowman, Clindy G.
APPLICANT: Bowman, Clindy G.
APPLICANT: Bowson, John L.
APPLICANT: Bowson, John L.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: SYNTHETIC DNA SECTIVITY IN MAIZE
MINMERD OR SECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||| | |||||: ||||: 690
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Patent No. 6075185
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US-08-459-504B-7
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487 576 547

Search completed: October 28, 2004, 18:34:24 Job time : 25.3343 secs